

<110> NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY  
AMERSHAM BIOSCIENCES KK

<120> Novel acetylgalactosamine transferases and nucleic acids encoding  
the same

<130> 159-86

<140> 10/524,505

<141> 2005-02-14

<150> PCT/JP03/10309

<151> 2003-08-13

<150> JP2002-236292

<151> 2002-08-14

<160> 34

<210> 1

<211> 1039

<212> PRT

<213> Homo sapiens

<400> 1

Met Pro Arg Leu Pro Val Lys Lys Ile Arg Lys Gln Met Lys Leu Leu  
1 5 10 15

Leu Leu Leu Leu Leu Leu Ser Cys Ala Ala Trp Leu Thr Tyr Val His  
20 25 30

Leu Gly Leu Val Arg Gln Gly Arg Ala Leu Arg Gln Arg Leu Gly Tyr  
35 40 45

Gly Arg Asp Gly Glu Lys Leu Thr Ser Glu Thr Asp Gly Arg Gly Val  
50 55 60

His Ala Ala Pro Ser Thr Gln Arg Ala Glu Asp Ser Ser Glu Ser Arg  
65 70 75 80

Glu Glu Glu Gln Ala Pro Glu Gly Arg Asp Leu Asp Met Leu Phe Pro  
85 90 95

Gly Gly Ala Gly Arg Leu Pro Leu Asn Phe Thr His Gln Thr Pro Pro  
100 105 110

Trp Arg Glu Glu Tyr Lys Gly Gln Val Asn Leu His Val Phe Glu Asp  
115 120 125

Trp Cys Gly Gly Ala Val Gly His Leu Arg Arg Asn Leu His Phe Pro  
130 135 140

Leu Phe Pro His Thr Arg Thr Thr Val Lys Lys Leu Ala Val Ser Pro

145		150		155		160
Lys Trp Lys Asn Tyr Gly Leu Arg Ile Phe Gly Phe Ile His Pro Ala						
	165			170		175
Arg Asp Gly Asp Val Gln Phe Ser Val Ala Ser Asp Asp Asn Ser Glu						
	180		185			190
Phe Trp Leu Ser Leu Asp Glu Ser Pro Ala Ala Ala Gln Leu Val Ala						
	195		200			205
Phe Val Gly Lys Thr Gly Ser Glu Trp Thr Ala Pro Gly Glu Phe Thr						
	210		215			220
Lys Phe Ser Ser Gln Val Ser Lys Pro Arg Arg Leu Met Ala Ser Arg						
225		230		235		240
Arg Tyr Tyr Phe Glu Leu Leu His Lys Gln Asp Asp Arg Gly Ser Asp						
	245		250			255
His Val Glu Val Gly Trp Arg Ala Phe Leu Pro Gly Leu Lys Phe Glu						
	260		265			270
Val Ile Ser Ser Ala His Ile Ser Leu Tyr Thr Asp Glu Ser Ala Leu						
	275		280			285
Lys Met Asp His Val Ala His Val Pro Gln Ser Pro Ala Ser His Val						
	290		295			300
Gly Gly Arg Pro Pro Gln Glu Glu Thr Ser Ala Asp Met Leu Arg Pro						
305		310		315		320
Asp Pro Arg Asp Thr Phe Phe Leu Thr Pro Arg Met Glu Ser Ser Ser						
	325		330			335
Leu Glu Asn Val Leu Glu Pro Cys Ala Tyr Ala Pro Thr Tyr Val Val						
	340		345			350
Lys Asp Phe Pro Ile Ala Arg Tyr Gln Gly Leu Gln Phe Val Tyr Leu						
	355		360			365
Ser Phe Val Tyr Pro Asn Asp Tyr Thr Arg Leu Thr His Met Glu Thr						
	370		375			380
Asp Asn Lys Cys Phe Tyr Arg Glu Ser Pro Leu Tyr Leu Glu Arg Phe						
385		390		395		400
Gly Phe Tyr Lys Tyr Met Lys Met Asp Lys Glu Glu Gly Asp Glu Asp						
	405		410			415
Glu Glu Asp Glu Val Gln Arg Arg Ala Phe Leu Phe Leu Asn Pro Asp						
	420		425			430
Asp Phe Leu Asp Asp Glu Asp Glu Gly Glu Leu Leu Asp Ser Leu Glu						
	435		440			445

Pro Thr Glu Ala Ala Pro Pro Arg Ser Gly Pro Gln Ser Pro Ala Pro  
 450 455 460

Ala Ala Pro Ala Gln Pro Gly Ala Thr Leu Ala Pro Pro Thr Pro Pro  
 465 470 475 480

Arg Pro Arg Asp Gly Gly Thr Pro Arg His Ser Arg Ala Leu Ser Trp  
 485 490 495

Ala Ala Arg Ala Ala Arg Pro Leu Pro Leu Phe Leu Gly Arg Ala Pro  
 500 505 510

Pro Pro Arg Pro Ala Val Glu Gln Pro Pro Pro Lys Val Tyr Val Thr  
 515 520 525

Arg Val Arg Pro Gly Gln Arg Ala Ser Pro Arg Ala Pro Ala Pro Arg  
 530 535 540

Ala Pro Trp Pro Pro Phe Pro Gly Val Phe Leu His Pro Arg Pro Leu  
 545 550 555 560

Pro Arg Val Gln Leu Arg Ala Pro Pro Arg Pro Pro Arg Pro His Gly  
 565 570 575

Arg Arg Thr Gly Gly Pro Gln Ala Thr Gln Pro Arg Pro Pro Ala Arg  
 580 585 590

Ala Gln Ala Thr Gln Gly Gly Arg Glu Gly Gln Ala Arg Thr Leu Gly  
 595 600 605

Pro Ala Ala Pro Thr Val Asp Ser Asn Leu Ser Ser Glu Ala Arg Pro  
 610 615 620

Val Thr Ser Phe Leu Ser Leu Ser Gln Val Ser Gly Pro Gln Leu Pro  
 625 630 635 640

Gly Glu Gly Glu Glu Glu Glu Gly Glu Asp Asp Gly Ala Pro Gly  
 645 650 655

Asp Glu Ala Ala Ser Glu Asp Ser Glu Glu Ala Ala Gly Pro Ala Leu  
 660 665 670

Gly Arg Trp Arg Glu Asp Ala Ile Asp Trp Gln Arg Thr Phe Ser Val  
 675 680 685

Gly Ala Val Asp Phe Glu Leu Leu Arg Ser Asp Trp Asn Asp Leu Arg  
 690 695 700

Cys Asn Val Ser Gly Asn Leu Gln Leu Pro Glu Ala Glu Ala Val Asp  
 705 710 715 720

Val Thr Ala Gln Tyr Met Glu Arg Leu Asn Ala Arg His Gly Gly Arg  
 725 730 735

Phe Ala Leu Leu Arg Ile Val Asn Val Glu Lys Arg Arg Asp Ser Ala  
 740 745 750

Arg Gly Ser Arg Phe Leu Leu Glu Leu Glu Leu Gln Glu Arg Gly Gly  
 755 760 765  
 Gly Arg Leu Arg Leu Ser Glu Tyr Val Phe Leu Arg Leu Pro Gly Ala  
 770 775 780  
 Arg Val Gly Asp Ala Asp Gly Glu Ser Pro Glu Pro Ala Pro Ala Ala  
 785 790 795 800  
 Ser Val Arg Pro Asp Gly Arg Pro Glu Leu Cys Arg Pro Leu Arg Leu  
 805 810 815  
 Ala Trp Arg Gln Asp Val Met Val His Phe Ile Val Pro Val Lys Asn  
 820 825 830  
 Gln Ala Arg Trp Val Ala Gln Phe Leu Ala Asp Met Ala Ala Leu His  
 835 840 845  
 Ala Arg Thr Gly Asp Ser Arg Phe Ser Val Val Leu Val Asp Phe Glu  
 850 855 860  
 Ser Glu Asp Met Asp Val Glu Arg Ala Leu Arg Ala Ala Arg Leu Pro  
 865 870 875 880  
 Arg Tyr Gln Tyr Leu Arg Arg Thr Gly Asn Phe Glu Arg Ser Ala Gly  
 885 890 895  
 Leu Gln Ala Gly Val Asp Ala Val Glu Asp Ala Ser Ser Ile Val Phe  
 900 905 910  
 Leu Cys Asp Leu His Ile His Phe Pro Pro Asn Ile Leu Asp Gly Ile  
 915 920 925  
 Arg Lys His Cys Val Glu Gly Arg Leu Ala Phe Ala Pro Val Val Met  
 930 935 940  
 Arg Leu Ser Cys Gly Ser Ser Pro Arg Asp Pro His Gly Tyr Trp Glu  
 945 950 955 960  
 Val Asn Gly Phe Gly Leu Phe Gly Ile Tyr Lys Ser Asp Phe Asp Arg  
 965 970 975  
 Val Gly Gly Met Asn Thr Glu Glu Phe Arg Asp Gln Trp Gly Gly Glu  
 980 985 990  
 Asp Trp Glu Leu Leu Asp Arg Val Leu Gln Ala Gly Leu Glu Val Glu  
 995 1000 1005  
 Arg Leu Arg Leu Arg Asn Phe Tyr His His Tyr His Ser Lys Arg Gly  
 1010 1015 1020  
 Met Trp Ser Val Arg Ser Arg Lys Gly Ser Arg Thr Gly Ala Ser  
 1025 1030 1035 1039

<210> 2

<211> 3120

<212> DNA

<213> Homo sapiens

<400> 2

atg ccg cgg ctc ccg gtg aag aag atc cgt aag cag atg aag ctg ctg	48
Met Pro Arg Leu Pro Val Lys Lys Ile Arg Lys Gln Met Lys Leu Leu	
1 5 10 15	
ctg ctg ctg ctg ctg ctg agc tgc gcc gcg tgg ctc acc tac gtg cac	96
Leu Leu Leu Leu Leu Leu Ser Cys Ala Ala Trp Leu Thr Tyr Val His	
20 25 30	
ctg ggc ctg gtg cgc cag gga cgc gcg ctg cgc cag cgc ctg ggc tac	144
Leu Gly Leu Val Arg Gln Gly Arg Ala Leu Arg Gln Arg Leu Gly Tyr	
35 40 45	
ggg cga gat ggt gag aag ctg acc agt gag acc gac ggc cgg ggg gtc	192
Gly Arg Asp Gly Glu Lys Leu Thr Ser Glu Thr Asp Gly Arg Gly Val	
50 55 60	
cac gct gcg cca tcc aca cag agg gct gag gac tcc agt gag agc cgt	240
His Ala Ala Pro Ser Thr Gln Arg Ala Glu Asp Ser Ser Glu Ser Arg	
65 70 75 80	
gaa gag gag caa gcg ccc gaa ggt cgg gac cta gac atg ctg ttt cct	288
Glu Glu Glu Gln Ala Pro Glu Gly Arg Asp Leu Asp Met Leu Phe Pro	
85 90 95	
ggg ggg gct ggg agg ctg cca ctg aac ttc acc cat cag aca ccc cca	336
Gly Gly Ala Gly Arg Leu Pro Leu Asn Phe Thr His Gln Thr Pro Pro	
100 105 110	
tgg cgg gag gag tac aag ggg cag gtg aac ctg cac gtg ttt gag gac	384
Trp Arg Glu Glu Tyr Lys Gly Gln Val Asn Leu His Val Phe Glu Asp	
115 120 125	
tgg tgt ggg ggc gcc gtg ggc cac ctg agg agg aac ctg cac ttc ccg	432
Trp Cys Gly Gly Ala Val Gly His Leu Arg Arg Asn Leu His Phe Pro	
130 135 140	
ctg ttc cct cat acg cgc acc acc gtg aag aag ttg gcc gtg tcc ccc	480
Leu Phe Pro His Thr Arg Thr Thr Val Lys Lys Leu Ala Val Ser Pro	
145 150 155 160	
aag tgg aag aac tat gga ctc cgt att ttt ggt ttc atc cac ccg gcg	528
Lys Trp Lys Asn Tyr Gly Leu Arg Ile Phe Gly Phe Ile His Pro Ala	
165 170 175	
agg gac gga gac gtc cag ttt tct gtg gcc tca gac gac aac tcg gag	576
Arg Asp Gly Asp Val Gln Phe Ser Val Ala Ser Asp Asp Asn Ser Glu	
180 185 190	
ttc tgg ctg agt ctg gac gag agc cct gct gct gcc cag ctt gtg gcc	624
Phe Trp Leu Ser Leu Asp Glu Ser Pro Ala Ala Ala Gln Leu Val Ala	
195 200 205	
ttt gtg ggc aag act ggc tcc gag tgg aca gcg cct gga gaa ttc acc	672

Phe	Val	Gly	Lys	Thr	Gly	Ser	Glu	Trp	Thr	Ala	Pro	Gly	Glu	Phe	Thr		
210						215					220						
aag	ttc	agc	tcc	cag	gtg	tcc	aag	ccc	agg	cgg	ctc	atg	gcc	tcc	cgg	720	
Lys	Phe	Ser	Ser	Gln	Val	Ser	Lys	Pro	Arg	Arg	Leu	Met	Ala	Ser	Arg		
225					230				235						240		
agg	tac	tac	ttt	gag	ttg	ctg	cac	aag	cag	gac	gac	cgc	ggc	tcg	gac	768	
Arg	Tyr	Tyr	Phe	Glu	Leu	Leu	His	Lys	Gln	Asp	Asp	Arg	Gly	Ser	Asp		
				245					250					255			
cac	gtg	gaa	gtg	ggc	tgg	cga	gct	ttc	ctg	ccc	ggc	ctg	aag	ttc	gag	816	
His	Val	Glu	Val	Gly	Trp	Arg	Ala	Phe	Leu	Pro	Gly	Leu	Lys	Phe	Glu		
			260					265					270				
gtc	atc	agc	tct	gct	cac	atc	tcc	ctg	tac	aca	gat	gag	tca	gcc	ttg	864	
Val	Ile	Ser	Ser	Ala	His	Ile	Ser	Leu	Tyr	Thr	Asp	Glu	Ser	Ala	Leu		
	275						280					285					
aag	atg	gac	cac	gtg	gcg	cac	gtc	ccc	cag	tct	cca	gcc	agc	cac	gtg	912	
Lys	Met	Asp	His	Val	Ala	His	Val	Pro	Gln	Ser	Pro	Ala	Ser	His	Val		
	290						295				300						
ggg	ggg	cgt	ccg	ccg	cag	gag	gag	acc	agc	gca	gac	atg	ctg	cgg	cca	960	
Gly	Gly	Arg	Pro	Pro	Gln	Glu	Glu	Thr	Ser	Ala	Asp	Met	Leu	Arg	Pro		
305					310					315					320		
gat	ccc	agg	gat	acc	ttt	ttc	ctc	act	cca	cgc	atg	gaa	tct	tcg	agc	1008	
Asp	Pro	Arg	Asp	Thr	Phe	Phe	Leu	Thr	Pro	Arg	Met	Glu	Ser	Ser	Ser		
				325					330					335			
ctg	gag	aac	gtg	ctg	gag	ccc	tgc	gcc	tac	gcc	ccc	acc	tac	gtg	gtc	1056	
Leu	Glu	Asn	Val	Leu	Glu	Pro	Cys	Ala	Tyr	Ala	Pro	Thr	Tyr	Val	Val		
			340					345					350				
aag	gac	ttc	ccg	atc	gcc	aga	tac	cag	ggc	ctg	caa	ttt	gtg	tac	ctg	1104	
Lys	Asp	Phe	Pro	Ile	Ala	Arg	Tyr	Gln	Gly	Leu	Gln	Phe	Val	Tyr	Leu		
	355						360					365					
tcc	ttc	gtt	tat	ccc	aac	gac	tac	act	cgc	ctc	acc	cac	atg	gag	acg	1152	
Ser	Phe	Val	Tyr	Pro	Asn	Asp	Tyr	Thr	Arg	Leu	Thr	His	Met	Glu	Thr		
	370					375					380						
gac	aac	aag	tgc	ttc	tac	cgc	gag	tct	ccg	ctg	tat	ctg	gag	agg	ttt	1200	
Asp	Asn	Lys	Cys	Phe	Tyr	Arg	Glu	Ser	Pro	Leu	Tyr	Leu	Glu	Arg	Phe		
385					390					395					400		
ggg	ttc	tat	aaa	tac	atg	aag	atg	gac	aag	gag	gag	ggg	gat	gag	gat	1248	
Gly	Phe	Tyr	Lys	Tyr	Met	Lys	Met	Asp	Lys	Glu	Gly	Asp	Glu	Asp			
			405					410					415				
gaa	gaa	gac	gag	gtg	cag	cgc	cga	gcc	ttc	ctc	ttc	ctc	aac	ccg	gac	1296	
Glu	Glu	Asp	Glu	Val	Gln	Arg	Arg	Ala	Phe	Leu	Phe	Leu	Asn	Pro	Asp		
			420					425					430				
gac	ttc	ctg	gac	gac	gag	gac	gag	ggg	gag	ctg	ctc	gac	agc	ctg	gag	1344	
Asp	Phe	Leu	Asp	Asp	Glu	Asp	Glu	Gly	Glu	Leu	Leu	Asp	Ser	Leu	Glu		

435	440	445	
ccc acc gag gcg gcc ccg ccc agg agc ggc ccc cag tcc ccc gcc cca Pro Thr Glu Ala Ala Pro Pro Arg Ser Gly Pro Gln Ser Pro Ala Pro 450 455 460			1392
gca gcc ccc gcc cag ccc gga gcc acc ctc gcc ccg ccg acc cct ccc Ala Ala Pro Ala Gln Pro Gly Ala Thr Leu Ala Pro Pro Thr Pro Pro 465 470 475 480			1440
cgc ccc cgg gac ggg ggg acc ccc agg cac tcc cgg gcc ctg agc tgg Arg Pro Arg Asp Gly Gly Thr Pro Arg His Ser Arg Ala Leu Ser Trp 485 490 495			1488
gcc gcc agg gcc gcc cgc cct ttg ccg ctc ttc ttg ggc cga gct ccg Ala Ala Arg Ala Ala Arg Pro Leu Pro Leu Phe Leu Gly Arg Ala Pro 500 505 510			1536
ccc ccg cgc cct gca gtg gag cag ccg ccc cca aag gtg tac gtg acc Pro Pro Arg Pro Ala Val Glu Gln Pro Pro Pro Lys Val Tyr Val Thr 515 520 525			1584
agg gtg cgg ccg gga cag cgg gca tcc ccc cgg gcc cca gcg ccg cgt Arg Val Arg Pro Gly Gln Arg Ala Ser Pro Arg Ala Pro Ala Pro Arg 530 535 540			1632
gcg ccc tgg ccg ccc ttc cct ggc gtc ttc ctg cac ccc agg cct ctg Ala Pro Trp Pro Pro Phe Pro Gly Val Phe Leu His Pro Arg Pro Leu 545 550 555 560			1680
ccc aga gtg cag ctg cgg gcg ccc cca cgc cca ccc cgg ccc cac ggc Pro Arg Val Gln Leu Arg Ala Pro Pro Arg Pro Pro Arg Pro His Gly 565 570 575			1728
cgc agg acc ggc ggc ccc cag gcc aca cag ccg agg ccc cca gcc cgg Arg Arg Thr Gly Gly Pro Gln Ala Thr Gln Pro Arg Pro Pro Ala Arg 580 585 590			1776
gcg cag gcc acc caa ggg ggc cgg gag ggc cag gcg cgc acg ctg gga Ala Gln Ala Thr Gln Gly Gly Arg Glu Gly Gln Ala Arg Thr Leu Gly 595 600 605			1824
cct gcg gcg ccc aca gtg gac tca aac ttg tcc tcc gaa gcg cgg ccc Pro Ala Ala Pro Thr Val Asp Ser Asn Leu Ser Ser Glu Ala Arg Pro 610 615 620			1872
gtg acc tcc ttc ctg agc ttg tcc cag gtg tcc ggg ccg cag ctg ccc Val Thr Ser Phe Leu Ser Leu Ser Gln Val Ser Gly Pro Gln Leu Pro 625 630 635 640			1920
ggg gag ggc gaa gag gag gag gaa ggg gag gac gat ggg gcc ccg ggc Gly Glu Gly Glu Glu Glu Glu Glu Gly Glu Asp Asp Gly Ala Pro Gly 645 650 655			1968
gac gag gcc gcg tcg gag gac agc gag gag gcc gcg ggc ccg gcg ctc Asp Glu Ala Ala Ser Glu Asp Ser Glu Glu Ala Ala Gly Pro Ala Leu 660 665 670			2016

gga cgc tgg cgt gag gac gcc atc gac tgg cag cgc acg ttc agc gtg	2064
Gly Arg Trp Arg Glu Asp Ala Ile Asp Trp Gln Arg Thr Phe Ser Val	
675 680 685	
ggc gcc gtg gac ttc gag ctg ctg cgc tcg gac tgg aac gac ctg cga	2112
Gly Ala Val Asp Phe Glu Leu Leu Arg Ser Asp Trp Asn Asp Leu Arg	
690 695 700	
tgc aac gtt tcg ggg aac ctg cag ctg ccg gag gcg gag gcc gtg gac	2160
Cys Asn Val Ser Gly Asn Leu Gln Leu Pro Glu Ala Glu Ala Val Asp	
705 710 715 720	
gtg acc gct cag tac atg gag cgg ctg aac gcg cgc cac ggc ggg cgc	2208
Val Thr Ala Gln Tyr Met Glu Arg Leu Asn Ala Arg His Gly Gly Arg	
725 730 735	
ttc gcg ctt ctg cgc atc gtg aac gtg gag aag cgc cgg gac tcg gcg	2256
Phe Ala Leu Leu Arg Ile Val Asn Val Glu Lys Arg Arg Asp Ser Ala	
740 745 750	
cga ggg agt cgc ttc ctg ctg gag ctg gag ctg cag gag cgc ggg ggc	2304
Arg Gly Ser Arg Phe Leu Leu Glu Leu Glu Leu Gln Glu Arg Gly Gly	
755 760 765	
ggc cgc ctg cga ctg tcc gag tac gtc ttc ctg cgg ctg ccg gga gcc	2352
Gly Arg Leu Arg Leu Ser Glu Tyr Val Phe Leu Arg Leu Pro Gly Ala	
770 775 780	
cgc gta ggg gat gca gac gga gaa agt ccc gaa ccc gct ccc gcc gcc	2400
Arg Val Gly Asp Ala Asp Gly Glu Ser Pro Glu Pro Ala Pro Ala Ala	
785 790 795 800	
tcc gtg cgc ccc gac ggc cgc ccc gag ctc tgc cgg cca ctg cgc ctg	2448
Ser Val Arg Pro Asp Gly Arg Pro Glu Leu Cys Arg Pro Leu Arg Leu	
805 810 815	
gcc tgg cgc cag gac gtg atg gtt cac ttc atc gtg cca gtg aaa aac	2496
Ala Trp Arg Gln Asp Val Met Val His Phe Ile Val Pro Val Lys Asn	
820 825 830	
cag gca cgg tgg gtg gca cag ttc ctg gcg gac atg gct gcg ctg cac	2544
Gln Ala Arg Trp Val Ala Gln Phe Leu Ala Asp Met Ala Ala Leu His	
835 840 845	
gcg cgc acc ggg gac tcg cgt ttc agc gtc gtc ctg gtg gat ttc gag	2592
Ala Arg Thr Gly Asp Ser Arg Phe Ser Val Val Leu Val Asp Phe Glu	
850 855 860	
agc gag gat atg gac gtg gag cgg gcc ctg cgc gcc gcg cgc ctg ccc	2640
Ser Glu Asp Met Asp Val Glu Arg Ala Leu Arg Ala Ala Arg Leu Pro	
865 870 875 880	
cgg tac cag tac ctg aga cga acc ggg aac ttc gag cgc tcc gcc ggg	2688
Arg Tyr Gln Tyr Leu Arg Arg Thr Gly Asn Phe Glu Arg Ser Ala Gly	
885 890 895	



ctg cag gcg gga gtg gac gcg gta gag gac gcc agc agc atc gtg ttc	2736
Leu Gln Ala Gly Val Asp Ala Val Glu Asp Ala Ser Ser Ile Val Phe	
900 905 910	
ctc tgc gac ctg cac atc cac ttc cca ccc aac atc ctg gac ggc atc	2784
Leu Cys Asp Leu His Ile His Phe Pro Pro Asn Ile Leu Asp Gly Ile	
915 920 925	
cgc aag cac tgc gtg gag ggc agg ctg gcc ttc gcg ccc gtg gtc atg	2832
Arg Lys His Cys Val Glu Gly Arg Leu Ala Phe Ala Pro Val Val Met	
930 935 940	
cgc ctg agc tgc ggg agc tcg ccc cgg gac ccc cac ggt tac tgg gag	2880
Arg Leu Ser Cys Gly Ser Ser Pro Arg Asp Pro His Gly Tyr Trp Glu	
945 950 955 960	
gtg aac ggc ttt ggc ctt ttt ggg atc tac aag tcg gac ttt gac cgg	2928
Val Asn Gly Phe Gly Leu Phe Gly Ile Tyr Lys Ser Asp Phe Asp Arg	
965 970 975	
gtt gga gga atg aac acg gag gag ttc cga gac cag tgg ggg ggt gaa	2976
Val Gly Gly Met Asn Thr Glu Glu Phe Arg Asp Gln Trp Gly Gly Glu	
980 985 990	
gac tgg gag ctc ctg gac agg gtc ctg cag gca ggg ctg gag gtg gag	3024
Asp Trp Glu Leu Leu Asp Arg Val Leu Gln Ala Gly Leu Glu Val Glu	
995 1000 1005	
cgg ctc cga ctg cgg aat ttc tat cac cac tac cac tcc aag agg ggc	3072
Arg Leu Arg Leu Arg Asn Phe Tyr His His Tyr His Ser Lys Arg Gly	
1010 1015 1020	
atg tgg agc gtc cgc agc agg aag ggc tct cgc acg ggg gcg tct tga	3120
Met Trp Ser Val Arg Ser Arg Lys Gly Ser Arg Thr Gly Ala Ser	
1025 1030 1035 1039	

<210> 3  
 <211> 998  
 <212> PRT  
 <213> Homo sapiens

<400> 3  
 Met Gly Ser Pro Arg Ala Ala Arg Pro Pro Leu Leu Leu Arg Pro Val  
 1 5 10 15  
 Lys Leu Leu Arg Arg Arg Phe Arg Leu Leu Leu Ala Leu Ala Val Val  
 20 25 30  
 Ser Val Gly Leu Trp Thr Leu Tyr Leu Glu Leu Val Ala Ser Ala Gln  
 35 40 45  
 Val Gly Gly Asn Pro Leu Asn Arg Arg Tyr Gly Ser Trp Arg Glu Leu  
 50 55 60  
 Ala Lys Ala Leu Ala Ser Arg Asn Ile Pro Ala Val Asp Pro His Leu  
 65 70 75 80

Gln	Phe	Tyr	His	Pro	Gln	Arg	Leu	Ser	Leu	Glu	Asp	His	Asp	Ile	Asp	85	90	95
Gln	Gly	Val	Ser	Ser	Asn	Ser	Ser	Tyr	Leu	Lys	Trp	Asn	Lys	Pro	Val	100	105	110
Pro	Trp	Leu	Ser	Glu	Phe	Arg	Gly	Arg	Ala	Asn	Leu	His	Val	Phe	Glu	115	120	125
Asp	Trp	Cys	Gly	Ser	Ser	Ile	Gln	Gln	Leu	Arg	Arg	Asn	Leu	His	Phe	130	135	140
Pro	Leu	Tyr	Pro	His	Ile	Arg	Thr	Thr	Leu	Arg	Lys	Leu	Ala	Val	Ser	145	150	155
Pro	Lys	Trp	Thr	Asn	Tyr	Gly	Leu	Arg	Ile	Phe	Gly	Tyr	Leu	His	Pro	165	170	175
Phe	Thr	Asp	Gly	Lys	Ile	Gln	Phe	Ala	Ile	Ala	Ala	Asp	Asp	Asn	Ala	180	185	190
Glu	Phe	Trp	Leu	Ser	Leu	Asp	Asp	Gln	Val	Ser	Gly	Leu	Gln	Leu	Leu	195	200	205
Ala	Ser	Val	Gly	Lys	Thr	Gly	Lys	Glu	Trp	Thr	Ala	Pro	Gly	Glu	Phe	210	215	220
Gly	Lys	Phe	Arg	Ser	Gln	Ile	Ser	Lys	Pro	Val	Ser	Leu	Ser	Ala	Ser	225	230	235
His	Arg	Tyr	Tyr	Phe	Glu	Val	Leu	His	Lys	Gln	Asn	Glu	Glu	Gly	Thr	245	250	255
Asp	His	Val	Glu	Val	Ala	Trp	Arg	Arg	Asn	Asp	Pro	Gly	Ala	Lys	Phe	260	265	270
Thr	Ile	Ile	Asp	Ser	Leu	Ser	Leu	Ser	Leu	Phe	Thr	Asn	Glu	Thr	Phe	275	280	285
Leu	Gln	Met	Asp	Glu	Val	Gly	His	Ile	Pro	Gln	Thr	Ala	Ala	Ser	His	290	295	300
Val	Asp	Ser	Ser	Asn	Ala	Leu	Pro	Arg	Asp	Glu	Gln	Pro	Pro	Ala	Asp	305	310	315
Met	Leu	Arg	Pro	Asp	Pro	Arg	Asp	Thr	Leu	Tyr	Arg	Val	Pro	Leu	Ile	325	330	335
Pro	Lys	Ser	His	Leu	Arg	His	Val	Leu	Pro	Asp	Cys	Pro	Tyr	Lys	Pro	340	345	350
Ser	Tyr	Leu	Val	Asp	Gly	Leu	Pro	Leu	Gln	Arg	Tyr	Gln	Gly	Leu	Arg	355	360	365
Phe	Val	His	Leu	Ser	Phe	Val	Tyr	Pro	Asn	Asp	Tyr	Thr	Arg	Leu	Ser	370	375	380

His	Met	Glu	Thr	His	Asn	Lys	Cys	Phe	Tyr	Gln	Glu	Asn	Ala	Tyr	Tyr	
385					390					395					400	
Gln	Asp	Arg	Phe	Ser	Phe	Gln	Glu	Tyr	Ile	Arg	Ile	Asp	Gln	Pro	Glu	
				405					410					415		
Lys	Gln	Gly	Leu	Glu	Gln	Pro	Gly	Phe	Glu	Glu	Asn	Leu	Leu	Glu	Glu	
			420					425					430			
Ser	Gln	Tyr	Gly	Glu	Val	Ala	Glu	Glu	Thr	Pro	Ala	Ser	Asn	Asn	Gln	
		435					440					445				
Asn	Ala	Arg	Met	Leu	Glu	Gly	Arg	Gln	Thr	Pro	Ala	Ser	Thr	Leu	Glu	
	450					455					460					
Gln	Asp	Ala	Thr	Asp	Tyr	Arg	Leu	Arg	Ser	Leu	Arg	Lys	Leu	Leu	Ala	
465					470					475					480	
Gln	Pro	Arg	Glu	Gly	Leu	Leu	Ala	Pro	Phe	Ser	Lys	Arg	Asn	Ser	Thr	
				485					490					495		
Ala	Ser	Phe	Pro	Gly	Arg	Thr	Ser	His	Ile	Pro	Val	Gln	Gln	Pro	Glu	
			500					505					510			
Lys	Arg	Lys	Gln	Lys	Pro	Ser	Pro	Glu	Pro	Ser	Gln	Asp	Ser	Pro	His	
		515					520					525				
Ser	Asp	Lys	Trp	Pro	Pro	Gly	His	Pro	Val	Lys	Asn	Leu	Pro	Gln	Met	
	530					535					540					
Arg	Gly	Pro	Arg	Pro	Arg	Pro	Ala	Gly	Asp	Ser	Pro	Arg	Lys	Thr	Gln	
545					550					555					560	
Trp	Leu	Asn	Gln	Val	Glu	Ser	Tyr	Ile	Ala	Glu	Gln	Arg	Arg	Gly	Asp	
				565					570					575		
Arg	Met	Arg	Pro	Gln	Ala	Pro	Gly	Arg	Gly	Trp	His	Gly	Glu	Glu	Glu	
			580					585					590			
Val	Val	Ala	Ala	Ala	Gly	Gln	Glu	Gly	Gln	Val	Glu	Gly	Glu	Glu	Glu	
		595					600					605				
Gly	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Met	Ser	Glu	Val	Phe	Glu	Tyr	
		610				615					620					
Val	Pro	Val	Phe	Asp	Pro	Val	Val	Asn	Trp	Asp	Gln	Thr	Phe	Ser	Ala	
625					630					635					640	
Arg	Asn	Leu	Asp	Phe	Gln	Ala	Leu	Arg	Thr	Asp	Trp	Ile	Asp	Leu	Ser	
				645					650					655		
Cys	Asn	Thr	Ser	Gly	Asn	Leu	Leu	Leu	Pro	Glu	Gln	Glu	Ala	Leu	Glu	
			660					665					670			
Val	Thr	Arg	Val	Phe	Leu	Lys	Lys	Leu	Asn	Gln	Arg	Ser	Arg	Gly	Arg	
			675				680						685			

Tyr	Gln	Leu	Gln	Arg	Ile	Val	Asn	Val	Glu	Lys	Arg	Gln	Asp	Gln	Leu	690	695	700	
Arg	Gly	Gly	Arg	Tyr	Leu	Leu	Glu	Leu	Glu	Leu	Leu	Glu	Gln	Gly	Gln	705	710	715	720
Arg	Val	Val	Arg	Leu	Ser	Glu	Tyr	Val	Ser	Ala	Arg	Gly	Trp	Gln	Gly	725	730	735	
Ile	Asp	Pro	Ala	Gly	Gly	Glu	Glu	Val	Glu	Ala	Arg	Asn	Leu	Gln	Gly	740	745	750	
Leu	Val	Trp	Asp	Pro	His	Asn	Arg	Arg	Arg	Gln	Val	Leu	Asn	Thr	Arg	755	760	765	
Ala	Gln	Glu	Pro	Lys	Leu	Cys	Trp	Pro	Gln	Gly	Phe	Ser	Trp	Ser	His	770	775	780	
Arg	Ala	Val	Val	His	Phe	Val	Val	Pro	Val	Lys	Asn	Gln	Ala	Arg	Trp	785	790	795	800
Val	Gln	Gln	Phe	Ile	Lys	Asp	Met	Glu	Asn	Leu	Phe	Gln	Val	Thr	Gly	805	810	815	
Asp	Pro	His	Phe	Asn	Ile	Val	Ile	Thr	Asp	Tyr	Ser	Ser	Glu	Asp	Met	820	825	830	
Asp	Val	Glu	Met	Ala	Leu	Lys	Arg	Ser	Lys	Leu	Arg	Ser	Tyr	Gln	Tyr	835	840	845	
Val	Lys	Leu	Ser	Gly	Asn	Phe	Glu	Arg	Ser	Ala	Gly	Leu	Gln	Ala	Gly	850	855	860	
Ile	Asp	Leu	Val	Lys	Asp	Pro	His	Ser	Ile	Ile	Phe	Leu	Cys	Asp	Leu	865	870	875	880
His	Ile	His	Phe	Pro	Ala	Gly	Val	Ile	Asp	Ala	Ile	Arg	Lys	His	Cys	885	890	895	
Val	Glu	Gly	Lys	Met	Ala	Phe	Ala	Pro	Met	Val	Met	Arg	Leu	His	Cys	900	905	910	
Gly	Ala	Thr	Pro	Gln	Trp	Pro	Glu	Gly	Tyr	Trp	Glu	Val	Asn	Gly	Phe	915	920	925	
Gly	Leu	Leu	Gly	Ile	Tyr	Lys	Ser	Asp	Leu	Asp	Arg	Ile	Gly	Gly	Met	930	935	940	
Asn	Thr	Lys	Glu	Phe	Arg	Asp	Arg	Trp	Gly	Gly	Glu	Asp	Trp	Glu	Leu	945	950	955	960
Leu	Asp	Arg	Ile	Leu	Gln	Ala	Gly	Leu	Asp	Val	Glu	Arg	Leu	Ser	Leu	965	970	975	
Arg	Asn	Phe	Phe	His	His	Phe	His	Ser	Lys	Arg	Gly	Met	Trp	Ser	Arg	980	985	990	

Arg Gln Met Lys Thr Leu  
 995 998

<210> 4  
 <211> 2997  
 <212> DNA  
 <213> Homo sapiens

<400> 4  
 atg ggg agc ccc cgg gcc gcg cgg ccc ccg ctg ctc ctg cgc ccg gtg 48  
 Met Gly Ser Pro Arg Ala Ala Arg Pro Pro Leu Leu Leu Arg Pro Val  
 1 5 10 15  
 aag ctg ctg cgg agg cgc ttc cgg ctg ctg ctg gcg ctc gcc gtg gtg 96  
 Lys Leu Leu Arg Arg Arg Phe Arg Leu Leu Leu Ala Leu Ala Val Val  
 20 25 30  
 tct gtg ggg ctc tgg act ctg tat ctg gaa ctg gtg gcg tcg gcc cag 144  
 Ser Val Gly Leu Trp Thr Leu Tyr Leu Glu Leu Val Ala Ser Ala Gln  
 35 40 45  
 gtc ggc ggg aac ccc ctg aac cgg agg tac ggc agc tgg aga gaa cta 192  
 Val Gly Gly Asn Pro Leu Asn Arg Arg Tyr Gly Ser Trp Arg Glu Leu  
 50 55 60  
 gcc aag gct ctg gcc agc agg aac att cca gct gtg gat cca cac ctc 240  
 Ala Lys Ala Leu Ala Ser Arg Asn Ile Pro Ala Val Asp Pro His Leu  
 65 70 75 80  
 cag ttc tac cat ccc cag agg ctg agc ctc gag gac cac gac att gac 288  
 Gln Phe Tyr His Pro Gln Arg Leu Ser Leu Glu Asp His Asp Ile Asp  
 85 90 95  
 caa ggg gtg agc agt aac agc agc tac ttg aag tgg aac aag cct gtc 336  
 Gln Gly Val Ser Ser Asn Ser Ser Tyr Leu Lys Trp Asn Lys Pro Val  
 100 105 110  
 ccc tgg ctc tca gag ttc cgg ggc cgt gcc aac ctg cat gtg ttt gaa 384  
 Pro Trp Leu Ser Glu Phe Arg Gly Arg Ala Asn Leu His Val Phe Glu  
 115 120 125  
 gac tgg tgt ggc agc tct atc cag cag ctc agg agg aac ctg cat ttc 432  
 Asp Trp Cys Gly Ser Ser Ile Gln Gln Leu Arg Arg Asn Leu His Phe  
 130 135 140  
 cca ctg tac ccc cat att cgc aca acc ctg agg aag ctt gct gtg tcc 480  
 Pro Leu Tyr Pro His Ile Arg Thr Thr Leu Arg Lys Leu Ala Val Ser  
 145 150 155 160  
 ccc aaa tgg acc aac tat ggc ctc cgc atc ttt ggc tac ctg cac ccc 528  
 Pro Lys Trp Thr Asn Tyr Gly Leu Arg Ile Phe Gly Tyr Leu His Pro  
 165 170 175  
 ttt act gat ggg aaa atc cag ttt gcc att gct gca gat gac aac gcg 576  
 Phe Thr Asp Gly Lys Ile Gln Phe Ala Ile Ala Ala Asp Asp Asn Ala

180	185	190	
gag ttc tgg ctg agc ctc gat Glu Phe Trp Leu Ser Leu Asp 195	gac cag gtc tca ggc ctc Asp Gln Val Ser Gly Leu 200	cag ctg ctg Gln Leu Leu 205	624
gcc agt gtg ggc aag act gga aag gag tgg acc gcc ccg gga gag ttt Ala Ser Val Gly Lys Thr Gly Lys Glu Trp Thr Ala Pro Gly Glu Phe 210 215 220			672
ggg aaa ttt cgg agc caa att tcc aag ccg gtg agc ctg tca gcc tcc Gly Lys Phe Arg Ser Gln Ile Ser Lys Pro Val Ser Leu Ser Ala Ser 225 230 235 240			720
cac agg tac tac ttc gag gtg ctg cac aag cag aat gag gag ggc acc His Arg Tyr Tyr Phe Glu Val Leu His Lys Gln Asn Glu Glu Gly Thr 245 250 255			768
gac cac gtg gaa gtt gca tgg cga cgg aac gac cct gga gcc aag ttc Asp His Val Glu Val Ala Trp Arg Arg Asn Asp Pro Gly Ala Lys Phe 260 265 270			816
acc atc att gac tcc ctc tcc ctg tcc ctc ttc aca aat gag acg ttc Thr Ile Ile Asp Ser Leu Ser Leu Ser Leu Phe Thr Asn Glu Thr Phe 275 280 285			864
cta cag atg gat gag gtg ggc cac atc cca cag aca gca gcc agc cac Leu Gln Met Asp Glu Val Gly His Ile Pro Gln Thr Ala Ala Ser His 290 295 300			912
gtg gac tcc tcc aac gct ctt ccc agg gat gag cag ccg ccc gct gac Val Asp Ser Ser Asn Ala Leu Pro Arg Asp Glu Gln Pro Pro Ala Asp 305 310 315 320			960
atg ctt cgg cct gac ccc cgg gac acc ctc tat cga gtg cct ctg atc Met Leu Arg Pro Asp Pro Arg Asp Thr Leu Tyr Arg Val Pro Leu Ile 325 330 335			1008
ccc aag tcg cat ctc cgc cac gtc ctg cct gac tgt ccc tac aaa ccc Pro Lys Ser His Leu Arg His Val Leu Pro Asp Cys Pro Tyr Lys Pro 340 345 350			1056
agc tat ctg gtg gat ggg ctt cct ctg cag cgc tac cag gga ctc cgg Ser Tyr Leu Val Asp Gly Leu Pro Leu Gln Arg Tyr Gln Gly Leu Arg 355 360 365			1104
ttt gtt cat ctg tct ttt gtt tac ccc aat gac tat acc cgc ctg agc Phe Val His Leu Ser Phe Val Tyr Pro Asn Asp Tyr Thr Arg Leu Ser 370 375 380			1152
cac atg gag acc cac aat aaa tgt ttc tac cag gaa aac gcc tac tac His Met Glu Thr His Asn Lys Cys Phe Tyr Gln Glu Asn Ala Tyr Tyr 385 390 395 400			1200
caa gac cgg ttc agc ttt cag gag tac atc agg att gac cag cct gag Gln Asp Arg Phe Ser Phe Gln Glu Tyr Ile Arg Ile Asp Gln Pro Glu 405 410 415			1248

aag cag ggg ctg gag cag cca ggt ttt gag gaa aac ctt cta gaa gag	1296
Lys Gln Gly Leu Glu Gln Pro Gly Phe Glu Glu Asn Leu Leu Glu Glu	
420 425 430	
tcc cag tat ggg gaa gtg gca gag gag acc cct gcc tcc aac aac cag	1344
Ser Gln Tyr Gly Glu Val Ala Glu Glu Thr Pro Ala Ser Asn Asn Gln	
435 440 445	
aat gcc agg atg ctt gag gga aga cag aca cct gcc tcc acc ctg gag	1392
Asn Ala Arg Met Leu Glu Gly Arg Gln Thr Pro Ala Ser Thr Leu Glu	
450 455 460	
caa gat gcc act gac tac cgc ctc cga agc ctg cgg aaa ctc ctg gct	1440
Gln Asp Ala Thr Asp Tyr Arg Leu Arg Ser Leu Arg Lys Leu Leu Ala	
465 470 475 480	
cag ccc cgg gag ggc ctg ctg gcc ccc ttc tcc aag cgg aac tcc aca	1488
Gln Pro Arg Glu Gly Leu Leu Ala Pro Phe Ser Lys Arg Asn Ser Thr	
485 490 495	
gcg tcc ttc cca ggg agg acc agc cac att cca gtg cag cag cca gag	1536
Ala Ser Phe Pro Gly Arg Thr Ser His Ile Pro Val Gln Gln Pro Glu	
500 505 510	
aag agg aag caa aaa ccc agc cct gag ccc agc caa gat tca cct cat	1584
Lys Arg Lys Gln Lys Pro Ser Pro Glu Pro Ser Gln Asp Ser Pro His	
515 520 525	
tcc gac aag tgg cct cct ggg cac cct gtg aag aac ctg cct cag atg	1632
Ser Asp Lys Trp Pro Pro Gly His Pro Val Lys Asn Leu Pro Gln Met	
530 535 540	
agg ggg ccc agg ccc agg ccc gct ggt gac agc ccc agg aag act cag	1680
Arg Gly Pro Arg Pro Arg Pro Ala Gly Asp Ser Pro Arg Lys Thr Gln	
545 550 555 560	
tgg ctg aac cag gtg gag tgg tac atc gca gag cag aga cgg ggt gac	1728
Trp Leu Asn Gln Val Glu Ser Tyr Ile Ala Glu Gln Arg Arg Gly Asp	
565 570 575	
agg atg cgg cct cag gcc ccc gga agg ggc tgg cat ggg gag gag gaa	1776
Arg Met Arg Pro Gln Ala Pro Gly Arg Gly Trp His Gly Glu Glu Glu	
580 585 590	
gtg gtg gcg gcc gca ggc cag gaa gga caa gtg gag gga gag gaa gag	1824
Val Val Ala Ala Ala Gly Gln Glu Gly Gln Val Glu Gly Glu Glu Glu	
595 600 605	
ggg gaa gaa gag gag gag gaa gag gat atg agt gag gtg ttc gag tac	1872
Gly Glu Glu Glu Glu Glu Glu Glu Glu Asp Met Ser Glu Val Phe Glu Tyr	
610 615 620	
gta cct gtg ttt gac ccg gta gta aac tgg gac cag acc ttc agt gcc	1920
Val Pro Val Phe Asp Pro Val Val Asn Trp Asp Gln Thr Phe Ser Ala	
625 630 635 640	

cgg aat ctc gac ttc caa gcc ctg agg act gac tgg atc gat ctg agc Arg Asn Leu Asp Phe Gln Ala Leu Arg Thr Asp Trp Ile Asp Leu Ser 645 650 655	1968
tgt aac aca tct ggc aac ctg ctg ctt cca gag cag gaa gct ctg gag Cys Asn Thr Ser Gly Asn Leu Leu Leu Pro Glu Gln Glu Ala Leu Glu 660 665 670	2016
gtc acg cga gtc ttc ttg aag aag ctc aac cag agg agc cgg ggg agg Val Thr Arg Val Phe Leu Lys Lys Leu Asn Gln Arg Ser Arg Gly Arg 675 680 685	2064
tac cag cta cag cgc att gtg aac gtg gaa aag cgt cag gac cag cta Tyr Gln Leu Gln Arg Ile Val Asn Val Glu Lys Arg Gln Asp Gln Leu 690 695 700	2112
cgt ggg ggt cgc tac ctc ctg gag ctt gaa ctg ttg gaa caa ggc cag Arg Gly Gly Arg Tyr Leu Leu Glu Leu Glu Leu Leu Glu Gln Gly Gln 705 710 715 720	2160
cgc gtg gtg cgg ctc tgc gag tat gtg tct gca cga ggc tgg cag ggc Arg Val Val Arg Leu Ser Glu Tyr Val Ser Ala Arg Gly Trp Gln Gly 725 730 735	2208
atc gat cca gct ggt ggg gag gag gtc gag gcc cgg aac ctg caa ggc Ile Asp Pro Ala Gly Gly Glu Glu Val Glu Ala Arg Asn Leu Gln Gly 740 745 750	2256
ctg gtc tgg gac cca cac aac cgt agg aga cag gtc ctg aat acc cgg Leu Val Trp Asp Pro His Asn Arg Arg Gln Val Leu Asn Thr Arg 755 760 765	2304
gcc caa gag ccc aag ctg tgc tgg cct cag ggt ttc tcc tgg agt cac Ala Gln Glu Pro Lys Leu Cys Trp Pro Gln Gly Phe Ser Trp Ser His 770 775 780	2352
cga gcc gtg gtc cac ttc gtc gtg cct gtg aag aac cag gca cgc tgg Arg Ala Val Val His Phe Val Val Pro Val Lys Asn Gln Ala Arg Trp 785 790 795 800	2400
gta cag caa ttc atc aaa gac atg gaa aac ctg ttc cag gtc acc ggt Val Gln Gln Phe Ile Lys Asp Met Glu Asn Leu Phe Gln Val Thr Gly 805 810 815	2448
gac cca cac ttc aac atc gtc atc act gac tat agc agt gag gac atg Asp Pro His Phe Asn Ile Val Ile Thr Asp Tyr Ser Ser Glu Asp Met 820 825 830	2496
gat gtt gag atg gca ctg aag agg tcc aag ctg cgg agc tac cag tac Asp Val Glu Met Ala Leu Lys Arg Ser Lys Leu Arg Ser Tyr Gln Tyr 835 840 845	2544
gtg aag cta agt gga aac ttt gaa cgc tca gct gga ctt cag gct ggc Val Lys Leu Ser Gly Asn Phe Glu Arg Ser Ala Gly Leu Gln Ala Gly 850 855 860	2592



ata gac ctc gtg aag gac ccg cac agc atc atc ttc ctc tgt gac ctc	2640
Ile Asp Leu Val Lys Asp Pro His Ser Ile Ile Phe Leu Cys Asp Leu	
865 870 875 880	
cac atc cac ttc cca gct gga gtc atc gat gcc att cgg aag cac tgt	2688
His Ile His Phe Pro Ala Gly Val Ile Asp Ala Ile Arg Lys His Cys	
885 890 895	
gtg gag gga aag atg gcc ttt gcc ccc atg gtg atg agg ctg cat tgt	2736
Val Glu Gly Lys Met Ala Phe Ala Pro Met Val Met Arg Leu His Cys	
900 905 910	
ggg gcc acc ccc cag tgg cct gag ggc tac tgg gag gtg aat ggg ttc	2784
Gly Ala Thr Pro Gln Trp Pro Glu Gly Tyr Trp Glu Val Asn Gly Phe	
915 920 925	
ggg ctg ctt ggc atc tac aag tct gac ctg gac agg att ggg ggc atg	2832
Gly Leu Leu Gly Ile Tyr Lys Ser Asp Leu Asp Arg Ile Gly Gly Met	
930 935 940	
aac acc aag gag ttc cga gac cgc tgg ggc ggg gaa gac tgg gag ctg	2880
Asn Thr Lys Glu Phe Arg Asp Arg Trp Gly Gly Glu Asp Trp Glu Leu	
945 950 955 960	
ctg gac agg ata ctc caa gcg ggc ctg gac gtg gag cgt ctc tcc ctc	2928
Leu Asp Arg Ile Leu Gln Ala Gly Leu Asp Val Glu Arg Leu Ser Leu	
965 970 975	
agg aat ttc ttc cat cat ttc cat tcc aag cga ggc atg tgg agc cgt	2976
Arg Asn Phe Phe His His Phe His Ser Lys Arg Gly Met Trp Ser Arg	
980 985 990	
cgc cag atg aag acg ctg tag	2997
Arg Gln Met Lys Thr Leu	
995 998	

<210> 5  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer used in PCR for cloning GalNAc-T1 cDNA

<400> 5  
 gctcctgcag ctccagctcc a 21

<210> 6  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer used in PCR for cloning GalNAc-T1 cDNA

<400> 6  
aagcgactcc ctcgcgccga gt 22

<210> 7  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T1 cDNA

<400> 7  
atgccgcggc tcccggtgaa gaag 24

<210> 8  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 8  
ccacagttca agctccagga ggta 24

<210> 9  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 9  
ctgacgcttt tccacgttca caat 24

<210> 10  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 10  
caccccgctct ctgctctgcg at 22

<210> 11  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 11  
gtcttctctgg ggctgtcacc a 21

<210> 12  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 12  
cacctcatcc atctgtagga acgt 24

<210> 13  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 13  
ctgtcgctg caacttccac gt 22

<210> 14  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 14  
aatgtcgtgg tcctcgaggc tca 23

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 15  
gatggtagaa ctggagggtgt ggat 24

<210> 16

<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T1 cDNA

<400> 16  
cccaagcttc ggggggtcca cgctgcgcca t 31

<210> 17  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T1 cDNA

<400> 17  
gctctagact caagacgccc ccgtgcgaga 30

<210> 18  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 18  
ggaattcgag gtacggcagc tggagagaa 29

<210> 19  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for cloning GalNAc-T2 cDNA

<400> 19  
acgcgtcgac ctacagcgtc ttcattctggc ga 32

<210> 20  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for amplifying GalNAc-T1 cDNA

<400> 20  
ctggtggatt tcgagagcga 20

<210> 21  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for amplifying GalNAc-T1 cDNA

<400> 21  
tgccgtccag gatgttgg 18

<210> 22  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide probe used in PCR for detecting GalNAc-T1 cDNA

<400> 22  
gcggtagagg acgcc 15

<210> 23  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for amplifying GalNAc-T2 cDNA

<400> 23  
atcgatcatca ctgactatag cagtga 26

<210> 24  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer used in PCR for amplifying GalNAc-T2 cDNA

<400> 24  
gaatggcatc gatgactcca g 21

<210> 25  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide probe used in PCR for detecting GalNAc-T2 cDNA

<400> 25  
ctcgtgaagg acccgca 17

<210> 26  
<211> 1034  
<212> PRT  
<213> Mouse

<400> 26  
Met Pro Trp Phe Pro Val Lys Lys Val Arg Lys Gln Met Lys Leu Leu  
1 5 10 15  
Leu Leu Leu Leu Leu Leu Thr Cys Ala Ala Trp Leu Thr Tyr Val His  
20 25 30  
Arg Ser Leu Val Arg Pro Gly Arg Ala Leu Arg Gln Arg Leu Gly Tyr  
35 40 45  
Gly Arg Asp Gly Glu Lys Leu Thr Gly Val Thr Asp Ser Arg Gly Val  
50 55 60  
Arg Val Pro Ser Ser Thr Gln Arg Ser Glu Asp Ser Ser Glu Ser His  
65 70 75 80  
Glu Glu Glu Gln Ala Pro Glu Gly Arg Gly Pro Asn Met Leu Phe Pro  
85 90 95  
Gly Gly Pro Arg Lys Pro Pro Pro Leu Asn Leu Thr His Gln Thr Pro  
100 105 110  
Pro Trp Arg Glu Glu Phe Lys Gly Gln Val Asn Leu His Val Phe Glu  
115 120 125  
Asp Trp Cys Gly Gly Ala Val Gly His Leu Arg Arg Asn Leu His Phe  
130 135 140  
Pro Leu Phe Pro His Thr Arg Thr Thr Val Thr Lys Leu Ala Val Ser  
145 150 155 160  
Pro Lys Trp Lys Asn Tyr Gly Leu Arg Ile Phe Gly Phe Ile His Pro  
165 170 175  
Ala Arg Asp Gly Asp Ile Gln Phe Ser Val Ala Ser Asp Asp Asn Ser  
180 185 190  
Glu Phe Trp Leu Ser Leu Asp Glu Ser Pro Ala Ala Ala Gln Leu Val  
195 200 205  
Ala Phe Val Gly Lys Thr Gly Ser Glu Trp Thr Ala Pro Gly Glu Phe  
210 215 220  
Thr Lys Phe Ser Ser Gln Val Ser Lys Pro Arg Arg Leu Met Ala Ser  
225 230 235 240  
Arg Arg Tyr Tyr Phe Glu Leu Leu His Lys Gln Asp Asp Lys Gly Ser

245										250					255				
Asp	His	Val	Glu	Val	Gly	Trp	Arg	Ala	Phe	Leu	Pro	Gly	Leu	Lys	Phe				
			260					265					270						
Glu	Ile	Ile	Asp	Ser	Ala	His	Ile	Ser	Leu	Tyr	Thr	Asp	Glu	Ser	Ser				
		275					280					285							
Leu	Lys	Met	Asp	His	Val	Ala	His	Val	Pro	Gln	Ser	Pro	Ala	Ser	His				
	290					295					300								
Ile	Gly	Gly	Phe	Pro	Pro	Gln	Gly	Glu	Pro	Ser	Ala	Asp	Met	Leu	His				
305					310						315				320				
Pro	Asp	Pro	Arg	Asp	Thr	Phe	Phe	Leu	Thr	Pro	Arg	Met	Glu	Pro	Leu				
				325					330					335					
Ser	Leu	Glu	Asn	Val	Leu	Glu	Pro	Cys	Ala	Tyr	Ala	Pro	Thr	Tyr	Ile				
			340					345					350						
Leu	Lys	Asp	Phe	Pro	Ile	Ala	Arg	Tyr	Gln	Gly	Leu	Gln	Phe	Val	Tyr				
		355					360					365							
Leu	Ser	Phe	Ile	Tyr	Pro	Asn	Asp	His	Thr	Arg	Leu	Thr	His	Met	Glu				
	370					375					380								
Thr	Asp	Asn	Lys	Cys	Phe	Tyr	Arg	Glu	Ser	Pro	Leu	Tyr	Leu	Glu	Arg				
385					390						395				400				
Phe	Gly	Phe	Tyr	Lys	Tyr	Met	Lys	Met	Asp	Lys	Glu	Glu	Gly	Glu	Glu				
				405					410					415					
Asp	Glu	Glu	Glu	Glu	Val	Gln	Arg	Arg	Ala	Phe	Leu	Phe	Leu	Asn	Pro				
			420					425					430						
Asp	Asp	Phe	Leu	Asp	Glu	Glu	Asp	Glu	Gln	Asp	Leu	Leu	Asp	Ser	Leu				
		435					440				445								
Glu	Pro	Thr	Asp	Ala	Ser	Val	Gln	Gln	Ser	His	Arg	Thr	Pro	Thr	Pro				
	450					455					460								
Ala	Ala	Ser	Thr	Gly	Thr	Thr	Ala	Ser	Pro	Thr	Pro	Pro	Thr	Thr	Ser				
465					470						475				480				
Pro	Leu	Asp	Glu	Gln	Thr	Leu	Arg	His	Ser	Arg	Ala	Leu	Asn	Trp	Ala				
				485					490				495						
Pro	Arg	Pro	Leu	Pro	Leu	Phe	Leu	Gly	Arg	Ala	Pro	Pro	Pro	Arg	Thr				
			500					505					510						
Val	Glu	Lys	Ser	Pro	Ser	Lys	Val	Tyr	Val	Thr	Arg	Val	Arg	Pro	Gly				
		515					520					525							
Gln	Arg	Ala	Ser	Pro	Arg	Ala	Leu	Arg	Asp	Ser	Pro	Trp	Pro	Pro	Phe				
	530					535					540								
Pro	Gly	Val	Phe	Leu	Arg	Pro	Lys	Pro	Leu	Pro	Arg	Val	Gln	Leu	Arg				

545		550		555		560									
Val	Pro	Pro	His	Pro	Pro	Arg	Thr	Gln	Gly	Tyr	Arg	Thr	Ser	Gly	Pro
				565					570					575	
Lys	Val	Thr	Glu	Leu	Lys	Pro	Pro	Val	Arg	Ala	Gln	Thr	Ser	Gln	Gly
			580					585					590		
Gly	Arg	Glu	Gly	Gln	Leu	His	Gly	Gln	Gly	Leu	Met	Val	Pro	Thr	Val
		595					600					605			
Asp	Leu	Asn	Ser	Ser	Val	Glu	Thr	Gln	Pro	Val	Thr	Ser	Phe	Leu	Ser
	610					615					620				
Leu	Ser	Gln	Val	Ser	Arg	Pro	Gln	Leu	Pro	Gly	Glu	Gly	Glu	Glu	Gly
625					630					635					640
Glu	Glu	Asp	Gly	Ala	Pro	Gly	Asp	Glu	Ala	Thr	Ser	Glu	Asp	Ser	Glu
				645					650					655	
Glu	Glu	Glu	Glu	Pro	Ala	Ala	Gly	Arg	Pro	Leu	Gly	Arg	Trp	Arg	Glu
			660					665					670		
Asp	Ala	Ile	Asn	Trp	Gln	Arg	Thr	Phe	Ser	Val	Gly	Ala	Met	Asp	Phe
	675					680					685				
Glu	Leu	Leu	Arg	Ser	Asp	Trp	Asn	Asp	Leu	Arg	Cys	Asn	Val	Ser	Gly
	690					695					700				
Asn	Leu	Gln	Leu	Pro	Glu	Ala	Glu	Ala	Val	Asp	Val	Val	Ala	Gln	Tyr
705				710						715					720
Met	Glu	Arg	Leu	Asn	Ala	Lys	His	Gly	Gly	Arg	Phe	Ser	Leu	Leu	Arg
				725					730					735	
Ile	Val	Asn	Val	Glu	Lys	Arg	Arg	Asp	Ser	Ala	Arg	Gly	Ser	Arg	Phe
		740						745					750		
Leu	Leu	Glu	Leu	Glu	Leu	Gln	Glu	Arg	Gly	Gly	Ser	Arg	Gln	Arg	Leu
		755					760					765			
Ser	Glu	Tyr	Val	Phe	Leu	Arg	Leu	Pro	Gly	Ala	Arg	Val	Gly	Asp	Glu
	770					775					780				
Asp	Gly	Glu	Ser	Pro	Glu	Pro	Pro	Pro	Ala	Ala	Ser	Ile	His	Pro	Asp
785				790						795					800
Ser	Arg	Pro	Glu	Leu	Cys	Arg	Pro	Leu	His	Leu	Ala	Trp	Arg	Gln	Asp
				805					810					815	
Val	Met	Val	His	Phe	Ile	Val	Pro	Val	Lys	Asn	Gln	Ala	Arg	Trp	Val
			820					825					830		
Val	Gln	Phe	Leu	Ala	Asp	Met	Thr	Ala	Leu	His	Val	His	Thr	Gly	Asp
		835					840					845			
Ser	Tyr	Phe	Asn	Ile	Ile	Leu	Val	Asp	Phe	Glu	Ser	Glu	Asp	Met	Asp



850	855	860
Val Glu Arg Ala Leu Arg Ala Ala Gln Leu Pro Arg Tyr Gln Tyr Leu 865 870 875 880		
Lys Arg Thr Gly Asn Phe Glu Arg Ser Ala Gly Leu Gln Thr Gly Val 885 890 895		
Asp Ala Val Glu Asp Pro Ser Ser Ile Val Phe Leu Cys Asp Leu His 900 905 910		
Ile His Phe Pro Pro Asn Ile Leu Asp Ser Ile Arg Lys His Cys Val 915 920 925		
Glu Gly Lys Leu Ala Phe Ala Pro Val Val Met Arg Leu Gly Cys Gly 930 935 940		
Ser Ser Pro Trp Asp Pro His Gly Tyr Trp Glu Val Asn Gly Phe Gly 945 950 955 960		
Leu Phe Gly Ile Tyr Lys Ser Asp Phe Asp Arg Val Gly Gly Met Asn 965 970 975		
Thr Glu Glu Phe Arg Asp Gln Trp Gly Gly Glu Asp Trp Glu Leu Leu 980 985 990		
Asp Arg Val Leu Gln Ala Gly Leu Glu Val Glu Arg Leu Arg Leu Arg 995 1000 1005		
His Phe Tyr His His Tyr His Ser Lys Arg Gly Met Trp Ala Thr Arg 1010 1015 1020		
Ser Arg Lys Gly Ala Arg Ala Gln Arg Ser 1025 1030		

<210> 27  
 <211> 3105  
 <212> DNA  
 <213> Mouse

<400> 27	
atg ccg tgg ttc ccg gtg aag aag gtc cgc aag cag atg aag ctg ctg Met Pro Trp Phe Pro Val Lys Lys Val Arg Lys Gln Met Lys Leu Leu 1 5 10 15	48
ctg ctg ttg ctg ctg ctc acc tgc gcc gcg tgg ctc acg tat gtg cac Leu Leu Leu Leu Leu Leu Thr Cys Ala Ala Trp Leu Thr Tyr Val His 20 25 30	96
cgg agc ctg gtg cgc ccg ggc cgc gcg cta cgc cag cgg ctg ggc tac Arg Ser Leu Val Arg Pro Gly Arg Ala Leu Arg Gln Arg Leu Gly Tyr 35 40 45	144
ggg cga gat ggg gag aag ctg acc ggt gtg acc gat agc cgc gga gtc Gly Arg Asp Gly Glu Lys Leu Thr Gly Val Thr Asp Ser Arg Gly Val 50 55 60	192

cga gtg cca tcg tcc aca cag agg tcg gag gac tcg agt gaa agt cat	240
Arg Val Pro Ser Ser Thr Gln Arg Ser Glu Asp Ser Ser Glu Ser His	
65 70 75 80	
gaa gag gag cag gcg ccc gag ggg cgg ggc cca aac atg ctg ttt cct	288
Glu Glu Glu Gln Ala Pro Glu Gly Arg Gly Pro Asn Met Leu Phe Pro	
85 90 95	
gga gga cct agg aag cca ccc cca ctg aac ctc acc cac cag aca ccc	336
Gly Gly Pro Arg Lys Pro Pro Pro Leu Asn Leu Thr His Gln Thr Pro	
100 105 110	
cca tgg cgg gaa gag ttc aaa gga cag gtg aac ctg cac gtg ttt gag	384
Pro Trp Arg Glu Glu Phe Lys Gly Gln Val Asn Leu His Val Phe Glu	
115 120 125	
gac tgg tgt gga ggt gct gtg ggc cac ctg aga cgg aat ctg cac ttc	432
Asp Trp Cys Gly Gly Ala Val Gly His Leu Arg Arg Asn Leu His Phe	
130 135 140	
cca ctc ttt cct cac act cgt act acg gtg aca aag tta gct gtg tcc	480
Pro Leu Phe Pro His Thr Arg Thr Thr Val Thr Lys Leu Ala Val Ser	
145 150 155 160	
cct aag tgg aag aac tat gga ctc cgg att ttt ggc ttc atc cac cca	528
Pro Lys Trp Lys Asn Tyr Gly Leu Arg Ile Phe Gly Phe Ile His Pro	
165 170 175	
gcc aga gat gga gac atc cag ttc tct gtg gct tcg gat gac aac tct	576
Ala Arg Asp Gly Asp Ile Gln Phe Ser Val Ala Ser Asp Asp Asn Ser	
180 185 190	
gag ttc tgg ctg agt ttg gat gag agc cca gca gcc gcc cag ctt gta	624
Glu Phe Trp Leu Ser Leu Asp Glu Ser Pro Ala Ala Ala Gln Leu Val	
195 200 205	
gcc ttt gtg ggc aag act ggc tcc gag tgg acc gca cct gga gaa ttc	672
Ala Phe Val Gly Lys Thr Gly Ser Glu Trp Thr Ala Pro Gly Glu Phe	
210 215 220	
acc aag ttc agc tcc cag gtg tct aag cca cgt cgg ctc atg gcc tcc	720
Thr Lys Phe Ser Ser Gln Val Ser Lys Pro Arg Arg Leu Met Ala Ser	
225 230 235 240	
cgg aga tac tac ttt gaa ctg ctc cac aag caa gat gac aag ggt tca	768
Arg Arg Tyr Tyr Phe Glu Leu Leu His Lys Gln Asp Asp Lys Gly Ser	
245 250 255	
gac cat gtg gaa gtg ggt tgg cga gct ttc ctg cct ggt ctg aag ttc	816
Asp His Val Glu Val Gly Trp Arg Ala Phe Leu Pro Gly Leu Lys Phe	
260 265 270	
gag atc att gat tct gct cac att tcc ctg tac aca gat gag tca tct	864
Glu Ile Ile Asp Ser Ala His Ile Ser Leu Tyr Thr Asp Glu Ser Ser	
275 280 285	

ctg aag atg gac cat gtg gcc cat gtg cct cag tct cca gcc agc cac Leu Lys Met Asp His Val Ala His Val Pro Gln Ser Pro Ala Ser His 290 295 300	912
ata gga gga ttc ccg ccg cag ggg gaa ccc agc gcc gac atg ctg cac Ile Gly Gly Phe Pro Pro Gln Gly Glu Pro Ser Ala Asp Met Leu His 305 310 315 320	960
cca gac ccc agg gat acc ttc ttc ctc act cct cgg atg gaa cct ttg Pro Asp Pro Arg Asp Thr Phe Phe Leu Thr Pro Arg Met Glu Pro Leu 325 330 335	1008
agc ctg gag aat gtt ctg gag ccc tgt gcc tat gcc ccc acc tat atc Ser Leu Glu Asn Val Leu Glu Pro Cys Ala Tyr Ala Pro Thr Tyr Ile 340 345 350	1056
ctc aag gat ttc ccc ata gcc aga tac caa gga cta cag ttt gtg tac Leu Lys Asp Phe Pro Ile Ala Arg Tyr Gln Gly Leu Gln Phe Val Tyr 355 360 365	1104
ctg tcc ttc atc tac ccc aat gac cat acc cgt ctc act cac atg gag Leu Ser Phe Ile Tyr Pro Asn Asp His Thr Arg Leu Thr His Met Glu 370 375 380	1152
aca gac aac aag tgc ttc tac cgt gag tcc cca cta tac ctg gaa agg Thr Asp Asn Lys Cys Phe Tyr Arg Glu Ser Pro Leu Tyr Leu Glu Arg 385 390 395 400	1200
ttt ggg ttc tat aaa tac atg aaa atg gac aag gag gag gga gag gaa Phe Gly Phe Tyr Lys Tyr Met Lys Met Asp Lys Glu Glu Gly Glu Glu 405 410 415	1248
gat gag gag gaa gaa gtt cag cgt aga gcc ttc ctc ttc ctc aac cca Asp Glu Glu Glu Glu Val Gln Arg Arg Ala Phe Leu Phe Leu Asn Pro 420 425 430	1296
gat gac ttc ctg gat gag gag gat gag cag gat ctg tta gac agc ctg Asp Asp Phe Leu Asp Glu Glu Asp Glu Gln Asp Leu Leu Asp Ser Leu 435 440 445	1344
gag ccc acc gat gca tct gta cag cag agc cac agg acc ccc acc cca Glu Pro Thr Asp Ala Ser Val Gln Gln Ser His Arg Thr Pro Thr Pro 450 455 460	1392
gca gcc tcc act gga acg aca gcc agc ccg acc cca cct aca act agt Ala Ala Ser Thr Gly Thr Thr Ala Ser Pro Thr Pro Pro Thr Thr Ser 465 470 475 480	1440
cct ctg gac gag cag acc ctc aga cac tcc cgg gca ctg aat tgg gcc Pro Leu Asp Glu Gln Thr Leu Arg His Ser Arg Ala Leu Asn Trp Ala 485 490 495	1488
cca cgc ccc ctg ccc ctc ttc ttg ggg cga gct cca cct ccc cga act Pro Arg Pro Leu Pro Leu Phe Leu Gly Arg Ala Pro Pro Pro Arg Thr 500 505 510	1536
gtg gag aag tcg cct tca aag gtg tac gtg acc agg gtc cga cct gga	1584

Val	Glu	Lys	Ser	Pro	Ser	Lys	Val	Tyr	Val	Thr	Arg	Val	Arg	Pro	Gly		
		515					520					525					
cag	cgg	gct	tcc	ccg	agg	gca	ttg	cga	gac	tca	ccc	tgg	cca	ccc	ttc	1632	
Gln	Arg	Ala	Ser	Pro	Arg	Ala	Leu	Arg	Asp	Ser	Pro	Trp	Pro	Pro	Phe		
	530					535					540						
cct	ggc	gtc	ttc	ctg	cgc	ccc	aag	cct	ctg	ccc	aga	gta	cag	ctg	cgg	1680	
Pro	Gly	Val	Phe	Leu	Arg	Pro	Lys	Pro	Leu	Pro	Arg	Val	Gln	Leu	Arg		
	545				550					555					560		
gta	ccc	cca	cat	cca	cct	cgg	acc	cag	ggc	tat	agg	acc	agt	ggc	ccc	1728	
Val	Pro	Pro	His	Pro	Pro	Arg	Thr	Gln	Gly	Tyr	Arg	Thr	Ser	Gly	Pro		
				565					570					575			
aag	gtc	aca	gaa	cta	aag	ccc	cca	gtc	agg	gcc	cag	acc	agc	cag	gga	1776	
Lys	Val	Thr	Glu	Leu	Lys	Pro	Pro	Val	Arg	Ala	Gln	Thr	Ser	Gln	Gly		
			580					585					590				
ggc	cgg	gag	ggc	cag	tta	cat	gga	cag	gga	ctc	atg	gtg	ccc	aca	gtg	1824	
Gly	Arg	Glu	Gly	Gln	Leu	His	Gly	Gln	Gly	Leu	Met	Val	Pro	Thr	Val		
	595						600					605					
gac	ttg	aac	tcc	tca	gtg	gaa	aca	cag	cct	gtg	act	tcc	ttc	ctg	agc	1872	
Asp	Leu	Asn	Ser	Ser	Val	Glu	Thr	Gln	Pro	Val	Thr	Ser	Phe	Leu	Ser		
	610					615					620						
ttg	tct	cag	gta	tcc	agg	cca	cag	ctg	cca	gga	gag	ggg	gaa	gaa	ggg	1920	
Leu	Ser	Gln	Val	Ser	Arg	Pro	Gln	Leu	Pro	Gly	Glu	Gly	Glu	Glu	Gly		
	625				630					635					640		
gag	gag	gat	ggg	gcc	cca	ggg	gat	gag	gcc	aca	tca	gaa	gac	agt	gag	1968	
Glu	Glu	Asp	Gly	Ala	Pro	Gly	Asp	Glu	Ala	Thr	Ser	Glu	Asp	Ser	Glu		
				645					650					655			
gaa	gag	gag	gag	ccg	gcc	gct	ggg	cgg	ccc	ctg	ggg	cgc	tgg	cgg	gag	2016	
Glu	Glu	Glu	Glu	Pro	Ala	Ala	Gly	Arg	Pro	Leu	Gly	Arg	Trp	Arg	Glu		
			660				665						670				
gat	gcc	atc	aac	tgg	cag	cgc	acg	ttc	agc	gtg	ggc	gcc	atg	gac	ttc	2064	
Asp	Ala	Ile	Asn	Trp	Gln	Arg	Thr	Phe	Ser	Val	Gly	Ala	Met	Asp	Phe		
	675					680						685					
gag	ctc	ctg	cgc	tct	gac	tgg	aac	gac	ctg	cgc	tgt	aac	gta	tcc	ggg	2112	
Glu	Leu	Leu	Arg	Ser	Asp	Trp	Asn	Asp	Leu	Arg	Cys	Asn	Val	Ser	Gly		
	690					695					700						
aac	ctg	caa	ctt	cct	gag	gcc	gaa	gcg	gtg	gat	gta	gtg	gct	cag	tac	2160	
Asn	Leu	Gln	Leu	Pro	Glu	Ala	Glu	Ala	Val	Asp	Val	Val	Ala	Gln	Tyr		
	705				710					715					720		
atg	gag	cgg	cta	aat	gca	aag	cat	ggc	ggg	cgc	ttc	tcg	ctt	cta	cgc	2208	
Met	Glu	Arg	Leu	Asn	Ala	Lys	His	Gly	Gly	Arg	Phe	Ser	Leu	Leu	Arg		
				725					730					735			
atc	gtg	aac	gtg	gag	aag	cgc	cgc	gac	tct	gca	cgc	ggg	agc	cgc	ttc	2256	
Ile	Val	Asn	Val	Glu	Lys	Arg	Arg	Asp	Ser	Ala	Arg	Gly	Ser	Arg	Phe		

740	745	750	
ctc ctg gaa ctg gaa ttg caa gag cgc gga ggg agc cgc cag cgc cta Leu Leu Glu Leu Glu Leu Gln Glu Arg Gly Gly Ser Arg Gln Arg Leu 755 760 765			2304
tcc gaa tac gtc ttc ctg cgg ttg ccc gga gcc cgc gtt ggg gac gaa Ser Glu Tyr Val Phe Leu Arg Leu Pro Gly Ala Arg Val Gly Asp Glu 770 775 780			2352
gat gga gaa agt ccc gag ccg cct cca gcc gcc tcg atc cac cca gac Asp Gly Glu Ser Pro Glu Pro Pro Pro Ala Ala Ser Ile His Pro Asp 785 790 795 800			2400
agt cgc cca gag ctc tgc cgg cct ttg cat ctg gcc tgg cgt cag gat Ser Arg Pro Glu Leu Cys Arg Pro Leu His Leu Ala Trp Arg Gln Asp 805 810 815			2448
gtc atg gtt cat ttc att gta cca gtg aag aat cag gcg cgc tgg gta Val Met Val His Phe Ile Val Pro Val Lys Asn Gln Ala Arg Trp Val 820 825 830			2496
gtg cag ttc ctg gca gat atg acc gcg ctg cat gtg cat acg ggg gac Val Gln Phe Leu Ala Asp Met Thr Ala Leu His Val His Thr Gly Asp 835 840 845			2544
tcg tac ttc aac atc atc ttg gtg gac ttt gag agc gag gac atg gat Ser Tyr Phe Asn Ile Ile Leu Val Asp Phe Glu Ser Glu Asp Met Asp 850 855 860			2592
gtg gag cgg gcc ctg cgt gcg gct cag cta cct cgg tac cag tac ttg Val Glu Arg Ala Leu Arg Ala Ala Gln Leu Pro Arg Tyr Gln Tyr Leu 865 870 875 880			2640
aaa cga act gga aac ttc gag cgc tct gca ggc ctg caa act gga gtg Lys Arg Thr Gly Asn Phe Glu Arg Ser Ala Gly Leu Gln Thr Gly Val 885 890 895			2688
gat gcc gtg gag gac ccc agc agc atc gtt ttc ctc tgt gac ctg cac Asp Ala Val Glu Asp Pro Ser Ser Ile Val Phe Leu Cys Asp Leu His 900 905 910			2736
atc cac ttc cca cct aat atc ctg gac agc atc cgc aag cat tgc gtg Ile His Phe Pro Pro Asn Ile Leu Asp Ser Ile Arg Lys His Cys Val 915 920 925			2784
gag ggc aag ctg gcc ttc gcc cct gtg gtc atg cgt ctg ggc tgt gga Glu Gly Lys Leu Ala Phe Ala Pro Val Val Met Arg Leu Gly Cys Gly 930 935 940			2832
agc tca ccg tgg gac cca cat ggt tac tgg gaa gtg aat gga ttt ggc Ser Ser Pro Trp Asp Pro His Gly Tyr Trp Glu Val Asn Gly Phe Gly 945 950 955 960			2880
ctc ttt ggg atc tac aaa tca gac ttt gac aga gta gga ggc atg aac Leu Phe Gly Ile Tyr Lys Ser Asp Phe Asp Arg Val Gly Gly Met Asn			2928

	965	970	975	
act gag gag ttc cgt gac cag tgg gga ggc gag gac tgg gaa ctt ctt				2976
Thr Glu Glu Phe Arg Asp Gln Trp Gly Gly Glu Asp Trp Glu Leu Leu				
	980	985	990	
gac agg gtc ctg cag gca ggg ctg gag gtg gag agg ctt cga ctg cga				3024
Asp Arg Val Leu Gln Ala Gly Leu Glu Val Glu Arg Leu Arg Leu Arg				
	995	1000	1005	
cac ttc tac cac cac tat cac tcg aag cga ggc atg tgg gcc aca cgc				3072
His Phe Tyr His His Tyr His Ser Lys Arg Gly Met Trp Ala Thr Arg				
	1010	1015	1020	
agc cgc aaa ggt gcc cgc gca cag cga tcc tga				3105
Ser Arg Lys Gly Ala Arg Ala Gln Arg Ser				
	1025	1030		
<210>	28			
<211>	986			
<212>	PRT			
<213>	Mouse			
<400>	28			
Met Gly Ser Pro Arg Ala Ala Leu Leu Met Leu Leu Leu Arg Pro Ile				
1 5 10 15				
Lys Leu Leu Arg Arg Arg Phe Arg Leu Leu Leu Leu Leu Ala Val Val				
20 25 30				
Ser Val Gly Leu Trp Thr Leu Tyr Leu Glu Leu Val Ala Ser Ala Gln				
35 40 45				
Ala Gly Gly Asn Pro Leu Asn His Arg Tyr Gly Ser Trp Arg Glu Leu				
50 55 60				
Ala Lys Ala Leu Ala Ser Arg Asn Ile Pro Ala Val Asp Pro Asn Leu				
65 70 75 80				
Gln Phe Tyr Arg Pro Gln Arg Leu Ser Leu Lys Asp Gln Glu Ile Ala				
85 90 95				
Arg Ser Arg Ser Arg Asn Ser Ser Tyr Leu Lys Trp Asn Lys Pro Val				
100 105 110				
Pro Trp Leu Ser Glu Phe Arg Gly His Ala Asn Leu His Val Phe Glu				
115 120 125				
Asp Trp Cys Gly Ser Ser Ile Gln Gln Leu Arg Asn Asn Leu His Phe				
130 135 140				
Pro Leu Tyr Pro His Ile Arg Thr Thr Leu Arg Lys Leu Ala Val Ser				
145 150 155 160				
Pro Lys Trp Thr Asn Tyr Gly Leu Arg Ile Phe Gly Tyr Leu His Pro				
165 170 175				

Phe	Thr	Asp	Gly	Lys	Ile	Gln	Phe	Ala	Ile	Ala	Ala	Asp	Asp	Asn	Ala		
			180					185					190				
Glu	Phe	Trp	Leu	Ser	Arg	Asp	Asp	Gln	Val	Ser	Gly	Leu	Gln	Leu	Leu		
		195					200					205					
Ala	Ser	Val	Gly	Lys	Thr	Gly	Lys	Glu	Trp	Thr	Ala	Pro	Gly	Glu	Phe		
		210				215					220						
Gly	Lys	Phe	Gln	Ser	Gln	Ile	Ser	Lys	Pro	Val	Ser	Leu	Ser	Ala	Ser		
225					230				235						240		
Leu	Arg	Tyr	Tyr	Phe	Glu	Val	Leu	His	Lys	Gln	Asn	Asp	Glu	Gly	Thr		
				245					250					255			
Asp	His	Val	Glu	Val	Ala	Trp	Arg	Arg	Asn	Asp	Pro	Gly	Ala	Lys	Phe		
			260					265					270				
Thr	Ile	Ile	Asp	Ser	Pro	Phe	Leu	Ser	Leu	Phe	Thr	Asn	Glu	Thr	Ile		
		275					280					285					
Leu	Arg	Met	Asp	Glu	Val	Gly	His	Ile	Pro	Gln	Thr	Ala	Ala	Ser	His		
		290				295					300						
Val	Gly	Ser	Ser	Asn	Thr	Pro	Pro	Arg	Asp	Glu	Gln	Pro	Pro	Ala	Asp		
305					310					315					320		
Met	Leu	Arg	Pro	Asp	Pro	Arg	Asp	Thr	Leu	Phe	Arg	Val	Pro	Leu	Ile		
				325					330					335			
Ala	Lys	Ser	His	Leu	Arg	His	Val	Leu	Pro	Asp	Cys	Pro	Tyr	Lys	Pro		
			340					345					350				
Ser	Tyr	Leu	Val	Asp	Gly	Leu	Pro	Leu	Gln	Arg	Tyr	Gln	Gly	Leu	Arg		
		355					360					365					
Phe	Val	His	Leu	Ser	Phe	Val	Tyr	Pro	Asn	Asp	Tyr	Thr	Arg	Leu	Ser		
		370				375					380						
His	Met	Glu	Thr	His	Asn	Lys	Cys	Phe	Tyr	Gln	Glu	Ser	Ala	Tyr	Asp		
385					390					395					400		
Gln	Asp	Arg	Ser	Ser	Phe	Gln	Glu	Tyr	Ile	Lys	Met	Asp	Lys	Pro	Glu		
				405					410					415			
Lys	His	Gly	Pro	Glu	Gln	Pro	Ala	Gly	Leu	Glu	Asp	Gly	Leu	Leu	Glu		
			420					425					430				
Glu	Ser	Gln	Tyr	Glu	Asp	Val	Pro	Glu	Glu	Ile	Pro	Thr	Ser	Gln	Asp		
		435					440					445					
Gln	Asn	Thr	Gly	Ile	Gln	Gly	Arg	Lys	Gln	Lys	Thr	Ile	Ser	Thr	Pro		
		450				455					460						
Gly	Leu	Gly	Val	Thr	Asp	Tyr	His	Leu	Arg	Lys	Leu	Leu	Ala	Arg	Ser		
465					470					475					480		

Gln	Ser	Gly	Pro	Val	Ala	Pro	Leu	Ser	Lys	Gln	Asn	Ser	Thr	Thr	Ala	
				485					490						495	
Phe	Pro	Thr	Arg	Thr	Ser	Asn	Ile	Pro	Val	Gln	Arg	Pro	Glu	Lys	Ser	
			500					505					510			
Pro	Val	Pro	Ser	Arg	Asp	Leu	Ser	His	Ser	Asp	Gln	Gly	Ala	Arg	Arg	
		515					520					525				
Asn	Leu	Pro	Leu	Ile	Gln	Arg	Ala	Arg	Pro	Thr	Gly	Asp	Arg	Pro	Gly	
	530					535					540					
Lys	Thr	Leu	Glu	Gln	Ser	Gln	Trp	Leu	Asn	Gln	Val	Glu	Ser	Phe	Ile	
545					550					555					560	
Ala	Glu	Gln	Arg	Arg	Gly	Asp	Arg	Ile	Glu	Pro	Pro	Thr	Pro	Ser	Arg	
				565					570					575		
Gly	Trp	Arg	Pro	Glu	Glu	Asp	Val	Val	Ile	Ala	Ala	Asp	Gln	Glu	Gly	
			580					585					590			
Glu	Val	Glu	Glu	Glu	Glu	Glu	Gly	Glu	Asp	Glu	Glu	Glu	Asp	Met	Ser	
		595					600					605				
Glu	Val	Phe	Glu	Tyr	Val	Pro	Met	Phe	Asp	Pro	Val	Val	Asn	Trp	Gly	
	610					615					620					
Gln	Thr	Phe	Ser	Ala	Gln	Asn	Leu	Asp	Phe	Gln	Ala	Leu	Arg	Thr	Asp	
625					630					635					640	
Trp	Ile	Asp	Leu	Asn	Cys	Asn	Thr	Ser	Gly	Asn	Leu	Leu	Leu	Pro	Glu	
				645					650					655		
Gln	Glu	Ala	Leu	Glu	Val	Thr	Arg	Val	Phe	Leu	Arg	Lys	Leu	Ser	Gln	
			660					665					670			
Arg	Thr	Arg	Gly	Arg	Tyr	Gln	Leu	Gln	Arg	Ile	Val	Asn	Val	Glu	Lys	
		675					680					685				
Arg	Gln	Asp	Arg	Leu	Arg	Gly	Gly	Arg	Tyr	Phe	Leu	Glu	Leu	Glu	Leu	
		690				695					700					
Leu	Asp	Gly	Gln	Arg	Leu	Val	Arg	Leu	Ser	Glu	Tyr	Val	Ser	Thr	Arg	
705					710					715					720	
Gly	Trp	Arg	Gly	Gly	Asp	His	Pro	Gly	Arg	Glu	Asp	Thr	Glu	Ala	Arg	
				725					730					735		
Asn	Leu	Gln	Gly	Leu	Val	Trp	Ser	Pro	Arg	Asn	Arg	His	Arg	His	Val	
			740					745					750			
Leu	Asn	Ala	Gln	Asp	Pro	Glu	Pro	Lys	Leu	Cys	Trp	Pro	Gln	Gly	Phe	
		755					760					765				
Ser	Trp	Asn	His	Arg	Ala	Val	Val	His	Phe	Ile	Val	Pro	Val	Lys	Asn	
	770					775					780					



Gln Ala Arg Trp Val Gln Gln Phe Ile Arg Asp Met Glu Ser Leu Ser  
 785 790 795 800  
 Gln Val Thr Gly Asp Ala His Phe Ser Ile Ile Ile Thr Asp Tyr Ser  
 805 810 815  
 Ser Glu Asp Met Asp Val Glu Met Ala Leu Lys Arg Ser Arg Leu Arg  
 820 825 830  
 Ser Tyr Gln Tyr Leu Lys Leu Ser Gly Asn Phe Glu Arg Ser Ala Gly  
 835 840 845  
 Leu Gln Ala Gly Ile Asp Leu Val Lys Asp Pro His Ser Ile Ile Phe  
 850 855 860  
 Leu Cys Asp Leu His Ile His Phe Pro Ala Gly Ile Ile Asp Thr Ile  
 865 870 875 880  
 Arg Lys His Cys Val Glu Gly Lys Met Ala Phe Ala Pro Met Val Met  
 885 890 895  
 Arg Leu His Cys Gly Ala Thr Pro Gln Trp Pro Glu Gly Tyr Trp Glu  
 900 905 910  
 Val Asn Gly Phe Gly Leu Leu Gly Ile Tyr Lys Ser Asp Leu Asp Lys  
 915 920 925  
 Ile Gly Gly Met Asn Thr Lys Glu Phe Arg Asp Arg Trp Gly Gly Glu  
 930 935 940  
 Asp Trp Glu Leu Leu Asp Arg Ile Leu Gln Ala Gly Leu Glu Val Glu  
 945 950 955 960  
 Arg Leu Ser Leu Arg Asn Phe Phe His His Phe His Ser Lys Arg Gly  
 965 970 975  
 Met Trp Asn Arg Arg Gln Met Lys Met Pro  
 980 985

<210> 29  
 <211> 2961  
 <212> DNA  
 <213> Mouse

<400> 29  
 atg ggg agc ccc cgc gcc gcg ttg ctg atg ctg ctc ctg cgc ccg atc 48  
 Met Gly Ser Pro Arg Ala Ala Leu Leu Met Leu Leu Leu Arg Pro Ile  
 1 5 10 15  
 aag ctg ctg agg agg cgc ttc cgg ctg ctg ctg ctg ctc gcc gta gta 96  
 Lys Leu Leu Arg Arg Arg Phe Arg Leu Leu Leu Leu Leu Ala Val Val  
 20 25 30  
 tcg gtg gga ctc tgg act ctg tat ctg gag ctg gtg gcg tcg gcc cag 144  
 Ser Val Gly Leu Trp Thr Leu Tyr Leu Glu Leu Val Ala Ser Ala Gln

35	40	45	
gcc ggc ggg aac ccc ctg aac cac agg tat ggc agc tgg cga gaa ctg Ala Gly Gly Asn Pro Leu Asn His Arg Tyr Gly Ser Trp Arg Glu Leu 50 55 60			192
gcc aag gcc cta gcc agc agg aac atc cca gcc gtt gat ccg aat ctc Ala Lys Ala Leu Ala Ser Arg Asn Ile Pro Ala Val Asp Pro Asn Leu 65 70 75 80			240
caa ttc tac cgt ccc cag cgg ctg agc ctc aag gac caa gaa att gcc Gln Phe Tyr Arg Pro Gln Arg Leu Ser Leu Lys Asp Gln Glu Ile Ala 85 90 95			288
cga agt agg agt agg aac agt agc tac ctg aag tgg aac aag cct gtc Arg Ser Arg Ser Arg Asn Ser Ser Tyr Leu Lys Trp Asn Lys Pro Val 100 105 110			336
ccc tgg ctc tca gag ttc cgg ggc cac gcc aac cta cat gtg ttt gaa Pro Trp Leu Ser Glu Phe Arg Gly His Ala Asn Leu His Val Phe Glu 115 120 125			384
gac tgg tgt ggc agc tcc atc caa cag ctg agg aac aac ctg cac ttc Asp Trp Cys Gly Ser Ser Ile Gln Gln Leu Arg Asn Asn Leu His Phe 130 135 140			432
cca ctc tac ccc cac atc cgc aca act ctg agg aag ctg gct gtg tcc Pro Leu Tyr Pro His Ile Arg Thr Thr Leu Arg Lys Leu Ala Val Ser 145 150 155 160			480
ccc aag tgg acc aac tat ggc ctc cgc ata ttt ggc tat ctg cac cct Pro Lys Trp Thr Asn Tyr Gly Leu Arg Ile Phe Gly Tyr Leu His Pro 165 170 175			528
ttc acc gat ggg aaa atc cag ttt gcc atc gct gct gat gac aat gct Phe Thr Asp Gly Lys Ile Gln Phe Ala Ile Ala Ala Asp Asp Asn Ala 180 185 190			576
gag ttc tgg ctg agt cgt gat gac cag gtc tca ggc ctt cag ctg ctg Glu Phe Trp Leu Ser Arg Asp Asp Gln Val Ser Gly Leu Gln Leu Leu 195 200 205			624
gcc agc gtg ggc aag aca gga aag gaa tgg aca gcc cct gga gag ttt Ala Ser Val Gly Lys Thr Gly Lys Glu Trp Thr Ala Pro Gly Glu Phe 210 215 220			672
ggg aaa ttt cag agt caa att tcc aag cca gtg agt tta tca gcc tcc Gly Lys Phe Gln Ser Gln Ile Ser Lys Pro Val Ser Leu Ser Ala Ser 225 230 235 240			720
ctc agg tac tac ttt gag gtc ctg cac aag caa aat gat gaa ggc act Leu Arg Tyr Tyr Phe Glu Val Leu His Lys Gln Asn Asp Glu Gly Thr 245 250 255			768
gac cac gtg gag gtc gcg tgg aga cgg aat gac cct gga gcc aag ttc Asp His Val Glu Val Ala Trp Arg Arg Asn Asp Pro Gly Ala Lys Phe 260 265 270			816

acc atc att gac tcc ccc ttc tta tct ctc ttt aca aat gag acc atc	864
Thr Ile Ile Asp Ser Pro Phe Leu Ser Leu Phe Thr Asn Glu Thr Ile	
275 280 285	
cta agg atg gat gag gtg ggc cat atc cca cag aca gca gcc agc cat	912
Leu Arg Met Asp Glu Val Gly His Ile Pro Gln Thr Ala Ala Ser His	
290 295 300	
gta ggc tcc tcc aac act cct ccc cgg gat gag cag ccc cca gct gac	960
Val Gly Ser Ser Asn Thr Pro Pro Arg Asp Glu Gln Pro Pro Ala Asp	
305 310 315 320	
atg ctg cgg cct gac cct cgg gac acc ctc ttt cga gtg cct ctg atc	1008
Met Leu Arg Pro Asp Pro Arg Asp Thr Leu Phe Arg Val Pro Leu Ile	
325 330 335	
gcc aag tcc cat ctg cgc cac gtc ctg ccc gat tgt ccc tac aaa ccc	1056
Ala Lys Ser His Leu Arg His Val Leu Pro Asp Cys Pro Tyr Lys Pro	
340 345 350	
agc tac ctg gtg gat gga ctc ccg cta cag cgc tac cag ggc ctc cgt	1104
Ser Tyr Leu Val Asp Gly Leu Pro Leu Gln Arg Tyr Gln Gly Leu Arg	
355 360 365	
ttt gtt cac ctg tcc ttt gtt tat ccc aat gac tat acc cgt ctg agc	1152
Phe Val His Leu Ser Phe Val Tyr Pro Asn Asp Tyr Thr Arg Leu Ser	
370 375 380	
cac atg gag acc cat aat aaa tgt ttc tac caa gaa agt gcc tat gac	1200
His Met Glu Thr His Asn Lys Cys Phe Tyr Gln Glu Ser Ala Tyr Asp	
385 390 395 400	
cag gac agg tcc agc ttc cag gaa tat atc aag atg gac aag cca gag	1248
Gln Asp Arg Ser Ser Phe Gln Glu Tyr Ile Lys Met Asp Lys Pro Glu	
405 410 415	
aag cat ggc ccg gag cag cca gca ggt ttg gag gat ggc ctt cta gaa	1296
Lys His Gly Pro Glu Gln Pro Ala Gly Leu Glu Asp Gly Leu Leu Glu	
420 425 430	
gaa tcc cag tat gaa gac gta cca gag gaa atc ccc acc tct caa gac	1344
Glu Ser Gln Tyr Glu Asp Val Pro Glu Glu Ile Pro Thr Ser Gln Asp	
435 440 445	
cag aat act ggg ata caa ggg aga aaa cag aag act att tcc acc ccg	1392
Gln Asn Thr Gly Ile Gln Gly Arg Lys Gln Lys Thr Ile Ser Thr Pro	
450 455 460	
ggg ctg ggt gtc act gac tac cac ctg cgg aag ctc ttg gct cgc tca	1440
Gly Leu Gly Val Thr Asp Tyr His Leu Arg Lys Leu Leu Ala Arg Ser	
465 470 475 480	
cag agt ggc cct gta gcg cct ctt tcc aaa cag aac tct aca act gcc	1488
Gln Ser Gly Pro Val Ala Pro Leu Ser Lys Gln Asn Ser Thr Thr Ala	
485 490 495	

ttt cca acc agg aca agc aac atc cca gtc cag cgg cca gag aaa agc	1536
Phe Pro Thr Arg Thr Ser Asn Ile Pro Val Gln Arg Pro Glu Lys Ser	
500 505 510	
cct gtg ccc agc cga gat ttg tct cat tct gac cag ggg gcc cgg agg	1584
Pro Val Pro Ser Arg Asp Leu Ser His Ser Asp Gln Gly Ala Arg Arg	
515 520 525	
aac ctg cct ctc atc cag aga gcc agg ccc act ggt gac aga cct ggg	1632
Asn Leu Pro Leu Ile Gln Arg Ala Arg Pro Thr Gly Asp Arg Pro Gly	
530 535 540	
aag act ctt gag cag tcc cag tgg ctg aat caa gtg gaa tcc ttc att	1680
Lys Thr Leu Glu Gln Ser Gln Trp Leu Asn Gln Val Glu Ser Phe Ile	
545 550 555 560	
gct gag cag aga agg gga gac agg ata gag cct cca acc ccc agc agg	1728
Ala Glu Gln Arg Arg Gly Asp Arg Ile Glu Pro Pro Thr Pro Ser Arg	
565 570 575	
ggc tgg cgt cct gag gag gac gtg gtg ata gcg gcg gac cag gaa gga	1776
Gly Trp Arg Pro Glu Glu Asp Val Val Ile Ala Ala Asp Gln Glu Gly	
580 585 590	
gaa gtg gag gag gag gaa gag ggg gaa gat gag gaa gaa gat atg agt	1824
Glu Val Glu Glu Glu Glu Glu Gly Glu Asp Glu Glu Glu Asp Met Ser	
595 600 605	
gag gtg ttc gaa tat gtg cct atg ttt gac cca gtg gtg aac tgg ggc	1872
Glu Val Phe Glu Tyr Val Pro Met Phe Asp Pro Val Val Asn Trp Gly	
610 615 620	
cag acc ttc agc gct cag aac ctc gac ttc caa gcc ctg aga acc gac	1920
Gln Thr Phe Ser Ala Gln Asn Leu Asp Phe Gln Ala Leu Arg Thr Asp	
625 630 635 640	
tgg atc gac ctg aac tgt aac aca tcg ggc aac ctg ctg ctt ccg gag	1968
Trp Ile Asp Leu Asn Cys Asn Thr Ser Gly Asn Leu Leu Leu Pro Glu	
645 650 655	
cag gag gcc ctg gag gtc aca cgg gtc ttc ctg aga aag ctc agc cag	2016
Gln Glu Ala Leu Glu Val Thr Arg Val Phe Leu Arg Lys Leu Ser Gln	
660 665 670	
agg acc cgg ggg aga tac cag ctg cag cgc att gtg aat gtg gag aag	2064
Arg Thr Arg Gly Arg Tyr Gln Leu Gln Arg Ile Val Asn Val Glu Lys	
675 680 685	
cgc cag gac cgg ctg cgc ggg ggg cgc tac ttc ctg gag ctt gaa ctg	2112
Arg Gln Asp Arg Leu Arg Gly Gly Arg Tyr Phe Leu Glu Leu Glu Leu	
690 695 700	
ctg gat ggc caa cgc ctg gta cgg ctc tcg gag tac gtg tcc act aga	2160
Leu Asp Gly Gln Arg Leu Val Arg Leu Ser Glu Tyr Val Ser Thr Arg	
705 710 715 720	
ggc tgg cgg gga ggt gac cac cca ggc agg gag gac aca gaa gct cgg	2208
Gly Trp Arg Gly Gly Asp His Pro Gly Arg Glu Asp Thr Glu Ala Arg	

725								730				735				
aac	ctg	cag	ggg	ctg	gtc	tgg	agc	cca	cgc	aac	cgt	cac	aga	cat	gtc	2256
Asn	Leu	Gln	Gly	Leu	Val	Trp	Ser	Pro	Arg	Asn	Arg	His	Arg	His	Val	
			740												750	
ctg	aat	gcc	cag	gat	cca	gag	ccc	aag	ctc	tgc	tgg	ccc	caa	ggg	ttc	2304
Leu	Asn	Ala	Gln	Asp	Pro	Glu	Pro	Lys	Leu	Cys	Trp	Pro	Gln	Gly	Phe	
			755												765	
tcc	tgg	aac	cat	cga	gct	gtg	gtc	cac	ttt	att	gtg	cct	gtg	aag	aac	2352
Ser	Trp	Asn	His	Arg	Ala	Val	Val	His	Phe	Ile	Val	Pro	Val	Lys	Asn	
			770												780	
cag	gct	cgc	tgg	gtg	cag	cag	ttc	atc	aga	gat	atg	gag	agc	ctg	tcc	2400
Gln	Ala	Arg	Trp	Val	Gln	Gln	Phe	Ile	Arg	Asp	Met	Glu	Ser	Leu	Ser	
			785												800	
caa	gtc	act	gga	gat	gca	cat	ttc	agc	atc	att	atc	aca	gac	tat	agc	2448
Gln	Val	Thr	Gly	Asp	Ala	His	Phe	Ser	Ile	Ile	Ile	Thr	Asp	Tyr	Ser	
			805												815	
agt	gag	gac	atg	gat	gtg	gag	atg	gct	ctg	aag	agg	tcc	aga	ctg	cgg	2496
Ser	Glu	Asp	Met	Asp	Val	Glu	Met	Ala	Leu	Lys	Arg	Ser	Arg	Leu	Arg	
			820												830	
agc	tac	cag	tac	ctg	aag	ctg	agt	gga	aac	ttt	gag	cgc	tct	gct	gga	2544
Ser	Tyr	Gln	Tyr	Leu	Lys	Leu	Ser	Gly	Asn	Phe	Glu	Arg	Ser	Ala	Gly	
			835												845	
ctg	cag	gct	ggc	ata	gac	ctg	gtg	aag	gat	cca	cac	agc	atc	atc	ttc	2592
Leu	Gln	Ala	Gly	Ile	Asp	Leu	Val	Lys	Asp	Pro	His	Ser	Ile	Ile	Phe	
			850												860	
ctc	tgt	gac	ctg	cac	atc	cac	ttt	cca	gca	gga	atc	att	gat	acc	atc	2640
Leu	Cys	Asp	Leu	His	Ile	His	Phe	Pro	Ala	Gly	Ile	Ile	Asp	Thr	Ile	
			865												880	
cgg	aag	cac	tgt	gtg	gag	ggc	aag	atg	gcc	ttt	gcc	ccc	atg	gtg	atg	2688
Arg	Lys	His	Cys	Val	Glu	Gly	Lys	Met	Ala	Phe	Ala	Pro	Met	Val	Met	
			885												895	
cgg	ctg	cac	tgt	ggg	gcc	acc	cca	cag	tgg	cct	gag	ggc	tac	tgg	gaa	2736
Arg	Leu	His	Cys	Gly	Ala	Thr	Pro	Gln	Trp	Pro	Glu	Gly	Tyr	Trp	Glu	
			900												910	
gta	aat	gga	ttt	gga	ctg	ctc	ggg	atc	tac	aag	tct	gac	ctg	gac	aag	2784
Val	Asn	Gly	Phe	Gly	Leu	Leu	Gly	Ile	Tyr	Lys	Ser	Asp	Leu	Asp	Lys	
			915												925	
atc	gga	ggc	atg	aac	acc	aag	gag	ttc	aga	gac	cgc	tgg	gga	ggg	gag	2832
Ile	Gly	Gly	Met	Asn	Thr	Lys	Glu	Phe	Arg	Asp	Arg	Trp	Gly	Gly	Glu	
			930												940	
gac	tgg	gag	ctg	ctg	gac	agg	att	ctc	caa	gca	ggc	ctg	gaa	gtg	gag	2880
Asp	Trp	Glu	Leu	Leu	Asp	Arg	Ile	Leu	Gln	Ala	Gly	Leu	Glu	Val	Glu	

945	950	955	960	
cgg ctc tcc ctc agg aac ttc ttc cat cac ttc cat tcc aag cga ggc				2928
Arg Leu Ser Leu Arg Asn Phe Phe His His Phe His Ser Lys Arg Gly				
	965	970	975	

atg tgg aac cgt cgc caa atg aag atg ccg tga	2961
Met Trp Asn Arg Arg Gln Met Lys Met Pro	
	980 985

<210> 30  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: FLAG peptide

<400> 30  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 31  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer used in PCR for amplifying  
 mNGalNAc-T1 cDNA

<400> 31  
 cccaagcttc gcctgggcta cgggcgagat 30

<210> 32  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer used in PCR for amplifying  
 mNGalNAc-T1 cDNA

<400> 32  
 gctctagact caggatcgct gtgcgcgggc a 31

<210> 33  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer used in PCR for amplifying

mNGalNAc-T2 cDNA

<400> 33

cccaagcttc ggcccaggcc ggcgggaacc 30

<210> 34

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used in PCR for amplifying  
mNGalNAc-T1 cDNA

<400> 34

ggaattctca cggcatcttc atttggcga 29